

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: January 9, 2003, 10:50:19 ; Search time 6156 seconds
(without alignments)
11213.752 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcaccgcgcgactgtgctg.....attacaggcatgaccaccg 2372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
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- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
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- 31: em_hgt_inv.*
- 32: em_hgt_other.*
- 33: em_hgt_mus.*
- 34: em_hgt_pln.*
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- 38: em_sy.*
- 39: em_hgtgo_hum.*
- 40: em_hgtgo_mus.*
- 41: em_hgtgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2372	100.0	2372	6	AR009781	Sequence AR009781
3	2372	100.0	2372	6	AR028963	Sequence AR028963
4	2372	100.0	2372	6	AR154584	Sequence AR154584
5	2372	100.0	2372	6	AR212312	Sequence AR212312
6	2372	100.0	2372	6	AX329941	Sequence AX329941
7	2372	100.0	2372	6	I11727	Sequence I11727
8	2372	100.0	2372	6	I12226	Sequence I12226
9	2372	100.0	2372	6	I21256	Sequence I21256
10	2372	100.0	2372	6	I25341	Sequence I25341
11	2372	100.0	2372	6	I36472	Sequence I36472
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18	1476	62.2	1476	6	A61359	Sequence A61359
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20	1302	54.9	1302	6	A44506	Sequence A44506
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22	1288.6	54.3	1477	4	AF322416	Sequence AF322416 Canis fam
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ALIGNMENTS

RESULT 1
AR000256
LOCUS AR000256 2372 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5736338.
ACCESSION AR000256
VERSION AR000256.1 GI:3962787
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B.
TITLE Method of diagnosing Neoplastic disease by detecting increased
expression of human MDM2 protein
JOURNAL Patent: US 5736338-A 2 07-APR-1998;

FEATURES
source Location/Qualifiers
1. .2372
BASE COUNT 698 a 491 c 541 g 642 t
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Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS AR009781 2372 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5756455.
ACCESSION AR009781
VERSION AR009781.1 GI:3968586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Kinzler,K.W. and Vogelstein,B.
TITLE Amplification of human MDM2 gene in human tumors
JOURNAL Patent: US 5756455-A 2 26-MAY-1998;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
ARI54584
LOCUS ARI54584 2372 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6238921.
ACCESSION ARI54584
VERSION ARI54584.1 GI:15122637
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 1 29-MAY-2001;
FEATURES Location/Qualifiers
 1..2372
 /organism="unknown"
BASE COUNT 698 a 491 c 541 g 642 t
ORIGIN

Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 AR212312
 LOCUS
 DEFINITION

Sequence 2 from patent US 6399755.
 AR212312 2372 bp DNA linear PAT 20-JUN-2002

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LOCUS AX329941 Sequence 450 from Patent WO0194629.
DEFINITION AX329941
ACCESSION AX329941
VERSION AX329941.1 GI:18102919
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrikan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 450 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	841	GTGAACGACAAAGAAACGCGCAAAATCTGATAGTATTTCCCTTTCCCTTTGATGAAGGCC	900
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Qy	1021	ATCAGGATTCAGTTTCAGATCAGTTTAGTGAGAAATTTGAAGTTGAATCTCTCGACTCAG	1080
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Db	1801	AAGGAAATATATATTTCTAACTATATAACCCCTAGGAAATTTAGACAACCTGAAATTTATTT	1860
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RESULT	8
LOCUS	I12226
DEFINITION	Sequence 1 from patent US 5420263.
ACCESSION	I12226
VERSION	I12226.1 GI:909724
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2372)
TITLE	Burrell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.
JOURNAL	Amplification of human MDM2 gene in human tumors
FEATURES	Patent: US 5420263-A 1 30-MAY-1995; Location/Qualifiers 1..2372 /organism="unknown"
BASE COUNT	698 a 491 c 541 g 642 t
ORIGIN	

	Query Match	100.0%	Score 2372:	DB 6:	Length 2372:
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RESULT 9

LOCUS 121256 2372 bp DNA linear PAT 07-OCT-1996

DEFINITION Sequence 1 from patent US 5519118.

ACCESSION 121256

VERSION 121256.1 GI:1601610

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Vogelstein,B. and Kinzler,K.

TITLE Human MDM2 protein involved in human tumors

JOURNAL Patent: US 5519118-A 1 21-MAY-1996;

FEATURES

Location/Qualifiers

1..2372

source

BASE COUNT 698 a 491 c 541 g 642 t

ORIGIN

Query Match 100.0%; Score 2372; DB 6; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCACCGCGCAGCTTGCTGCTCTCGGGCCCTGTGCGCCCTGTGTCGGAAAGATGGA 60

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Qy 121 CAGCAGGAGCAGCTCCCTCCCGGATAGTCGCTACGAGCGCCAGTCCCGCTGCGCCG 180

Db 121 CAGCAGGAGCAGCTCCCTCCCGGATAGTCGCTACGAGCGCCAGTCCCGCTGCGCCG 180

Qy 181 GAGAGTGGAAATGATCCCGAGGCCCGCGCGCTGCTCTCCGAGTAGTCACTCCCGCTG 240

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RESULT 10
 LOCUS I25341 2372 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 2 from patent US 5550023.
 ACCESSION I25341
 VERSION I25341.1 GI:1605211
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2372)
 AUTHORS Kinzler,K.W. and Vogelstein,B.
 TITLE Amplification of human MDM2 gene in human tumors
 JOURNAL Patent: US 5550023-A 2 27-AUG-1996;
 FEATURES Location/Qualifiers
 source 1..2372
 BASE COUNT 698 a 491 c 541 g 642 t
 ORIGIN
 Query Match 100.0%; Score 2372; DB 6; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
LOCUS I79856 2372 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 2 from patent US 5708136.
ACCESSION I79856
VERSION I79856.1 GI:3208146
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2372)
AUTHORS Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B.
TITLE Polypeptides which bind to human MDM2
JOURNAL Patent: US 5708136-A 2 13-JAN-1998;
FEATURES
Source 1..2372
BASE COUNT 698 a 491 c 541 g 642 t
ORIGIN
Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
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Query Match									
Best Local Similarity 100.0%; Score 2372; DB 9; Length 2372;									
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	1021	ATCAGGATTCAGTTTCAGATCAGTTTAGTGTAGAAATTTGAAGTTGAATCTCTCGACTCAG	1080						
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QY	1081	AAGATTATAGCTTTAGTGAAGAAGACAAAGCTCTCAGATGAAGATGATGAGGTATATC	1140						
DB	1081	AAGATTATAGCTTTAGTGAAGAAGACAAAGCTCTCAGATGAAGATGATGAGGTATATC	1140						
QY	1141	AAGTTACTGTGTATCAGCGAGGGAGAGTGATACAGATTCATTTTGAAGAAGATCCTGAAA	1200						
DB	1141	AAGTTACTGTGTATCAGCGAGGGAGAGTGATACAGATTCATTTTGAAGAAGATCCTGAAA	1200						
QY	1201	TTTCCTTAGCTGACTATTGGAAATGCACCTCATGCAATGAATGAATCCGCCCTTCCTAT	1260						
DB	1201	TTTCCTTAGCTGACTATTGGAAATGCACCTCATGCAATGAATGAATCCGCCCTTCCTAT	1260						
QY	1261	CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCTGGAAGATAAAGGGAAG	1320						
DB	1261	CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCTGGAAGATAAAGGGAAG	1320						
QY	1321	ATAAAGGGGAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAAGCTGAAGAGGCT	1380						
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DB	1381	TTGATGTTCTCTGATTGTAAGAAACTATAGTGAATGATTCAGAGAGTCTATGCTTTCAGG	1440						
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DB	1741	TATGTAGACAAACCAATTCAAATGATTTGCTAACTATTTCCTCTAGTTGACCTGTCTAT	1800						
QY	1801	AAGAGAAATATATTTCTAACTATATAACCTTAGGAATTTAGACAACTGAAAATTTATT	1860						
DB	1801	AAGAGAAATATATTTCTAACTATATAACCTTAGGAATTTAGACAACTGAAAATTTATT	1860						
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DB	1861	CACATATATCAAGTGAGAAAATGCTCAATTCACATAGATTTCTCTTTTACTATAAT	1920						
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DB	1921	TGACCTACTTTGGTAGTGAATAGTGAATACTTACTATAATTTGACTTGAATATGTAGCT	1980						
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DB	1981	CATCCTTTACACCAACTCCTAAATTTAAATAATTTTCTACTCTGTCTTAAATGAGAAATAC	2040						
QY	2041	TTGGTTTTTTTTTTCTTAAATATGATGACATTTAAATGATACTTATATTTTTTTTG	2100						
DB	2041	TTGGTTTTTTTTTTCTTAAATATGATGACATTTAAATGATACTTATATTTTTTTTG	2100						
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|||||
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Db 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTTAGTAGAGACAGGGTTTC 2280
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Db 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372

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Search completed: January 9, 2003, 12:43:32
Job time : 6162 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2003, 10:48:59 ; Search time 490 seconds
(without alignments)
10901.510 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcacgcgcgcgcgttgctg.....attacggcatgagccacgcg 2372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2372	100.0	2372	14	AAQ49891 Human MDM2 gene.
2	2372	100.0	2372	16	AAQ4589 Human MDM2 gene.
3	2372	100.0	2372	17	AAQ45151 Human MDM2-2 gene c
4	2372	100.0	2372	18	AAQ66410 Human MDM2 coding
5	2372	100.0	2372	18	AAQ62065 Human MDM2 cDNA.
6	2372	100.0	2372	19	AAQ28876 Human MDM2 gene.
7	2372	100.0	2372	19	AAQ20549 Human MDM2 encodin
8	2372	100.0	2372	19	AAQ04836 cDNA sequence of h
9	2372	100.0	2372	19	AAQ03607

10	2372	100.0	2372	20	AAQ37471 Human sarcoma p53-
11	2372	100.0	2372	20	AAQ35093 Nucleotide sequenc
12	2372	100.0	2372	20	AAQ03947 Human MDM2 encodin
13	2372	100.0	2372	21	AAQ29389 MDM2 oncoprotein c
14	2372	100.0	2372	22	AAQ29240 Human mdm2 cDNA se
15	2372	100.0	2372	22	AAQ07530 Human p-53 associat
16	2372	100.0	2372	22	AAQ80625 Human mdm2 cDNA.
17	2372	100.0	2372	24	AAQ43913 Human Dm2 (Hdm2) g
18	2372	100.0	2372	24	AAQ62113 Colon adenocarcino
19	2360.8	99.5	3190	22	AAQ51460 Human polynucleoti
20	2177	91.8	2393	23	AAQ4144 DNA encoding novel
21	1476	62.2	1476	18	AAQ61637 Murine double minu
22	1476	62.2	1476	22	AAQ84596 Human MDM2 protein
23	1397.4	58.9	1787	23	AAQ94139 DNA encoding novel
24	1371.8	57.8	1863	23	AAQ94143 DNA encoding novel
25	1302	54.9	1302	16	AAQ87263 Human double minut
26	1302	54.9	1302	16	AAQ92517 Human double minut
27	1161	48.9	1553	23	AAQ94140 DNA encoding novel
28	975.6	41.1	1710	14	AAQ49892 Murine MDM2 gene.
29	975.6	41.1	1710	16	AAQ94590 Murine MDM-2 gene
30	975.6	41.1	1710	17	AAQ45152 Murine MDM2 coding
31	975.6	41.1	1710	18	AAQ66411 Mouse MDM2 gene.
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34	975.6	41.1	1710	19	AAQ04885 cDNA sequence of m
35	975.6	41.1	1710	20	AAQ35104 Nucleotide sequenc
36	975.6	41.1	1710	20	AAQ03948 Mouse MDM2 encodin
37	975.6	41.1	1710	24	AAQ43912 Mouse Dm2 (Mdm2) g
38	975.6	41.1	1710	24	AAQ43912 Mouse ischaemic co
39	975.6	41.1	1710	24	AAQ199343 DNA encoding novel
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41	852	35.9	852	16	AAQ87261 Human double minut
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43	812.4	34.2	891	18	AAQ71254 Human mdm2-A gene.
44	812.4	34.2	891	21	AAQ60816 Nucleotide sequenc
45	812.2	34.2	966	18	AAQ71256 Human mdm2-C gene.

ALIGNMENTS

RESULT 1
AAQ49891
ID AAQ49891 standard; cDNA; 2372 BP.

AC AAQ49891;

DT 05-MAY-1994 (first entry)

DE Human MDM2 gene.

KW p53 gene; tumour suppressor gene; regulation; cellular proliferation;
KW cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
KW gene amplification; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 312..1787

FT /*tag= a

FT /product= Human MDM2

PN WO9320238-A.

XX 14-OCT-1993.

XX 07-APR-1993; 93WO-US03199.

PR 07-APR-1992; 92US-0867840.

PR 23-JUN-1992; 92US-0903103.

PA (UJJO) UNIV JOHNS HOPKINS.

PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;
XX WPI: 1993-336944/42.
DR P-PSDB; AAR42175.
XX Diagnosing neoplasia from amplification of MDM2 gene - or
PT elevated gene expression, also new DNA, MDM2 protein, antibodies
PT and treatment of sarcoma by inhibiting MDM2 expression
XX Claim 19; Fig 1; 75pp; English.
XX This sequence represents the MDM2 gene. Amplification of this gene is
CC diagnostic of neoplasia or the potential for neoplasia. The protein
CC encoded by this gene interacts with the product of the p53 gene. p53
CC is a tumour suppressor gene and encodes a protein which appears to be
CC a member of a group of proteins which regulate normal cellular
CC proliferation and suppression of cellular transformation. Inactivation of
CC of the p53 gene has been implicated in the formation, or progression of
CC a wide variety of carcinoma. Polypeptides containing at least amino
CC acids 13-41 of p53, or the DNA encoding these, may be used to inhibit
CC the growth of tumour cells containing MDM2 gene amplification.
XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
SQ
Query Match 100.0%; Score 2372; DB 14; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GCACCGCGGAGCTGGCTCTCTGGGGCTGTGTGGCCCTGTGTGCGGAAGATGA 60
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RESULT 2
 ID AAQ94589 standard; cDNA; 2372 BP.
 AC AAQ94589;
 DT 01-NOV-1995 (first entry)
 XX Human MDM2 gene.
 DE
 XX MDM2; sarcoma; diagnostic; DNA probe; ds.
 KW
 XX Homo sapiens (cell line CaCo-2).
 OS
 XX key Location/Qualifiers
 FH CDS 312..1784
 FT /*tag= a
 XX
 PN U55420263-A.
 XX
 PD 30-MAY-1995.
 XX
 PF 07-APR-1993; 93US-0044619.
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 PR 07-APR-1993; 93US-0044619.
 PR 07-APR-1992; 92US-0867840.
 PR 23-JUN-1992; 92US-0903103.
 XX
 PA (UJO) UNIV JOHNS HOPKINS.
 XX

PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;
 XX WPI; 1995-206312/27.
 DR P-PSDB; AAR76696.
 XX
 PT New human MDM2 cDNA - used to develop prods. for use in the
 PT diagnosis and treatment of tumours.
 XX
 PS Claim 1; Column 19-24; 34pp; English.
 XX
 CC The human MDM2 gene is genetically altered (i.e. amplified) in
 CC human tumour cells. Detecting that the gene has become
 CC amplified or detecting increased gene product expression (using
 CC probes, proteins, antibodies and inhibitors) allows diagnosis and
 CC therapy of cancers such as colorectal carcinoma, lung cancer and
 CC chronic myelogenous leukaemia. The human MDM2 protein binds to
 CC human p53 and allows the cell to escape from p53-regulated growth.
 XX
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
 Query Match 100.0%; Score 2372; DB 16; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 301 GGAGCAGGCAATGTCCATATACCAATGTCTGTACTTACTGTATGATGGTCTGTAAACCACT 360
 Db 301 GGAGCAGGCAATGTCCATATACCAATGTCTGTACTTACTGTATGATGGTCTGTAAACCACT 360
 QY 361 CACAGATTCCAGCTTCGGAAACAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGT 420
 Db 361 CACAGATTCCAGCTTCGGAAACAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGT 420
 QY 421 TATTAAGTCTGTGTGTCACAAAGACACCTATATCTATGAAAGAGGTTCTTTTATC 480
 Db 421 TATTAAGTCTGTGTGTCACAAAGACACCTATATCTATGAAAGAGGTTCTTTTATC 480
 QY 481 TTGCCAGTATATATGACTTAACGATTTATGATGAGAGCAACAACTATTTGATATT 540
 Db 481 TTGCCAGTATATATGACTTAACGATTTATGATGAGAGCAACAACTATTTGATATT 540
 QY 541 GTTCAAATGATCTCTAGGAGATTTGTTGGCGTCCAGCTTCTCTGTGAAAGAGCACA 600
 Db 541 GTTCAAATGATCTCTAGGAGATTTGTTGGCGTCCAGCTTCTCTGTGAAAGAGCACA 600
 QY 601 GGAAATATATACATGATCTACAGGAATCTGTGTAGTAGTCAATCAGCAGGAATCATCGG 660
 Db 601 GGAAATATATACATGATCTACAGGAATCTGTGTAGTAGTCAATCAGCAGGAATCATCGG 660
 QY 661 ACTCAGGTACATCTGTGAGTGAACAGAGTGTACCTTTGAAGTGGGAGTGTATCAAAAGG 720
 Db 661 ACTCAGGTACATCTGTGAGTGAACAGAGTGTACCTTTGAAGTGGGAGTGTATCAAAAGG 720
 QY 721 ACCTTGTACAGAGCTTCAGGAGAGAAACCTTCATCTCAGATTTGTTTCTTAGACCAT 780

Db	721	ACCTTGTACAAAGAGCTTCAGGAAGAGAACCCTTCATCTTCACATTTGGTTTCTAGACCAT	780
Qy	781	CTACCTCATCTAGAAGGAGAGCAAAATAGTGTGACACAGAAGAAAATTCAGATGAATATATCTG	840
Db	781	CTACCTCATCTAGAAGGAGAGCAAAATAGTGTGACACAGAAGAAAATTCAGATGAATATATCTG	840
Qy	841	GTGAAGCAAAAGAAAACCCGCAAAATCTGTATGTATTTCCCTTTTCCTTTGATGAAAGCC	900
Db	841	GTGAAGCAAAAGAAAACCCGCAAAATCTGTATGTATTTCCCTTTTCCTTTGATGAAAGCC	900
Qy	901	TGGCTCTGTGTGTAATAAGGGAGATATGTGTGTGAAGAAGCAGTAGCAGATGAATCTACAG	960
Db	901	TGGCTCTGTGTGTAATAAGGGAGATATGTGTGTGAAGAAGCAGTAGCAGATGAATCTACAG	960
Qy	961	GGACGCCATCGAAATCCGGATCTTGATGCTGGTGTAAAGTGAACATTCAGGTGATGGTGG	1020
Db	961	GGACGCCATCGAAATCCGGATCTTGATGCTGGTGTAAAGTGAACATTCAGGTGATGGTGG	1020
Qy	1021	ATCAGGATTCAGTTTCAGATCATGTTTACTGTGTAGATTTGAAGTTTGAATCTCTCGACCTCAG	1080
Db	1021	ATCAGGATTCAGTTTCAGATCATGTTTACTGTGTAGATTTGAAGTTTGAATCTCTCGACCTCAG	1080
Qy	1081	AAGATTATAGCCTTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGAGGTATATTC	1140
Db	1081	AAGATTATAGCCTTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGAGGTATATTC	1140
Qy	1141	AAGTTACTGTGTATCAGGCAGGGAGAGTGATACAGATTCAITTTGAAGAGATCCTCGAAA	1200
Db	1141	AAGTTACTGTGTATCAGGCAGGGAGAGTGATACAGATTCAITTTGAAGAGATCCTCGAAA	1200
Qy	1201	TTTCCTTAGCTGACTATTGGAAATGCATCTCATGCAATGAAATCAATCCGCCCTTCCTCAT	1260
Db	1201	TTTCCTTAGCTGACTATTGGAAATGCATCTCATGCAATGAAATCAATCCGCCCTTCCTCAT	1260
Qy	1261	CACATTGCAACAGATGTTGGGCCCTTCGTGTGAGAAATGGCTTCCTGGAAGATAAGGGAAAG	1320
Db	1261	CACATTGCAACAGATGTTGGGCCCTTCGTGTGAGAAATGGCTTCCTGGAAGATAAGGGAAAG	1320
Qy	1321	ATAAAGGGGAATCTCTGAGAAGCCAAACTTGAAAACTCAACACAAAGCTGGAAGAGGGCT	1380
Db	1321	ATAAAGGGGAATCTCTGAGAAGCCAAACTTGAAAACTCAACACAAAGCTGGAAGAGGGCT	1380
Qy	1381	TTGATGTTCTGTGATGTAAAAAACTATAGTGAATGATTTCCAGAGAGTCAATGTGTGAGG	1440
Db	1381	TTGATGTTCTGTGATGTAAAAAACTATAGTGAATGATTTCCAGAGAGTCAATGTGTGAGG	1440
Qy	1441	AAAAATGATGATAAAATTCACAAAGCTTCACAACTCACAGAAGTGAAGACTATCTTCAGC	1500
Db	1441	AAAAATGATGATAAAATTCACAAAGCTTCACAACTCACAGAAGTGAAGACTATCTTCAGC	1500
Qy	1501	CATCAACTCTTAGTAGCATTTATTTATAGCCGCAAGAGATGTGAAAGAGTTTGAAGGG	1560
Db	1501	CATCAACTCTTAGTAGCATTTATTTATAGCCGCAAGAGATGTGAAAGAGTTTGAAGGG	1560
Qy	1561	AAGAAACCCCAAGCAAGAAGAGATGTGGAATCTAGTTTGCCTTTAATGCCATTTGAAC	1620
Db	1561	AAGAAACCCCAAGCAAGAAGAGATGTGGAATCTAGTTTGCCTTTAATGCCATTTGAAC	1620
Qy	1621	CTTGTGTGATTTGCTCAAGGTCGACCTTAAAAATGGTTGCATTTGCCATGGCAAAACAGGAC	1680
Db	1621	CTTGTGTGATTTGCTCAAGGTCGACCTTAAAAATGGTTGCATTTGCCATGGCAAAACAGGAC	1680
Qy	1681	ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAGAAAGAAATAAGCCCTGCCAG	1740
Db	1681	ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAGAAAGAAATAAGCCCTGCCAG	1740
Qy	1741	TATGTAGACAAACCAATTCAAATGATGTGCTTAACCTATATTTCCCTCTAGCTGACCTGCTAT	1800
Db	1741	TATGTAGACAAACCAATTCAAATGATGTGCTTAACCTATATTTCCCTCTAGCTGACCTGCTAT	1800
Qy	1801	AAGAGAAATATATATTTCTTAACCTATATACCCCTAGGAATTTAGACAAACCTCGAAATTTAT	1860

Db	1801	AAGAGAAATTATATATTCTTAACCTATATAACCCCTAGGAATTTAGACAACCTCAAAATTTATT	1860	
QY	1861	CACATATATCAAGTAGAGAAAATGCCTCAATTCACATAGATTTCTTCTTTAGTATAAAT	1920	
Db	1861	CACATATATCAAGTAGAGAAAATGCCTCAATTCACATAGATTTCTTCTTTAGTATAAAT	1920	
QY	1921	TGACCTACTTTGGTAGTGGAAATAGTGAATACATTACTATAAATTTGACTTGAATATGTAGCT	1980	
Db	1921	TGACCTACTTTGGTAGTGGAAATAGTGAATACATTACTATAAATTTGACTTGAATATGTAGCT	1980	
QY	1981	CATCCTTTACACCAACATCCCTAAATTTTAAATAAATTTCTACTCTGTCTTAAATGAGAAAGTAC	2040	
Db	1981	CATCCTTTACACCAACATCCCTAAATTTTAAATAAATTTCTACTCTGTCTTAAATGAGAAAGTAC	2040	
QY	2041	TGCGTTTTTTTTTCTTAAATATGTATATGACATTTAAATGTAACTTATATTTTTTTTG	2100	
Db	2041	TGCGTTTTTTTTTCTTAAATATGTATATGACATTTAAATGTAACTTATATTTTTTTTG	2100	
QY	2101	AGACCGAGTCTTCCTCNGTTTACCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA	2160	
Db	2101	AGACCGAGTCTTCCTCNGTTTACCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA	2160	
QY	2161	AGCTCTGCCTCCCGGGTTTCGCACCATTTCTCCTGCCTCAGCCTCCCAATTTAGCTTGGCC	2220	
Db	2161	AGCTCTGCCTCCCGGGTTTCGCACCATTTCTCCTGCCTCAGCCTCCCAATTTAGCTTGGCC	2220	
QY	2221	TACAGTCACTTGCACACACACTGGCTAAATTTTTTGTACTTTTAGTAGAGACAGGGTTTC	2280	
Db	2221	TACAGTCACTTGCACACACACTGGCTAAATTTTTTGTACTTTTAGTAGAGACAGGGTTTC	2280	
QY	2281	ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCCTCC	2340	
Db	2281	ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCCTCC	2340	
QY	2341	CAAAAGTCGTGGATTCAGGCATGAGCCACCG	2372	
Db	2341	CAAAAGTCGTGGATTCAGGCATGAGCCACCG	2372	
RESULT 3				
AAAT45151				
ID	AAAT45151 standard; cDNA; 2372 BP.			
XX	AC	AAAT45151;		
XX	DT	28-JAN-1997 (first entry)		
DE	Human MDM-2 gene cDNA clone, involved in tumour-development.			
XX	p53; MDM-2; binding-inhibitor; identification; tumour; cancer;			
KW	neoplasia; antibody fusion protein; therapy; ds.			
XX	Homo sapiens.			
XX	Key	Location/Qualifiers		
PH	CDS	312..1787		
FT	/*tag= a			
XX	US5550023-A.			
XX	27-AUG-1996.			
XX	07-APR-1992;	92US-0867840.		
XX	07-APR-1993;	93US-0044619.		
PR	07-APR-1992;	92US-0867840.		
PR	23-JUN-1992;	92US-0903103.		
PR	18-MAY-1994;	94US-0245500.		
XX	(UYJO) UNIV JOHNS HOPKINS.			
FA	Kinzler KW, Vogelstein B;			
PI				
XX				

DR WPI: 1996-401591/40.
 DR P-PSDB: AAW07887.
 XX Identification of cpds. interfering with human MDM2/p53 binding -
 PT useful as therapeutic agents to treat human neoplastic cells
 XX
 PS Example 1; Column 21-26; 36pp; English.
 XX
 CC R4T45151 is a cDNA clone of the human MDM-2 gene derived from a human
 CC colon carcinoma cell line CaCo-2. The MDM-2 protein produced by
 CC this clone is used in a method for identifying compounds that
 CC interfere with the binding of p53 and MDM-2. In binding the p53
 CC protein, the MDM-2 protein releases a cell from p53-regulated growth,
 CC allowing cancers to develop. Therefore compounds identified as
 CC interfering with the binding of MDM-2 to p53 are potentially useful
 CC in the treatment of human neoplastic cells. In the method pref. One
 CC or both of the proteins is a fusion protein esp. with an antibody or
 CC antibody fragment which aids separation and identification.
 XX
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
 Query Match 100.0%; Score 2372; DB 17; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCACCGCGAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGGCGAAGATGGA 60
 DB 1 GCACCGCGAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGGCGAAGATGGA 60
 QY 61 GCAAGACCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 DB 61 GCAAGACCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 QY 121 CAGCCAGGAGCAGCGCTCCCTCCCGGATTAGTGCCTACGAGCGCCAGTGCCTGGCCCG 180
 DB 121 CAGCCAGGAGCAGCGCTCCCTCCCGGATTAGTGCCTACGAGCGCCAGTGCCTGGCCCG 180
 QY 181 GAGAGTGAATATCCCGAGGCGCCAGGCGCGTGTGTGGCGGCGGCGGCGGCGGCGGCG 240
 DB 181 GAGAGTGAATATCCCGAGGCGCCAGGCGCGTGTGTGGCGGCGGCGGCGGCGGCGGCG 240
 QY 241 AAGCAACTGGGAGCTTGGAGGCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 300
 DB 241 AAGCAACTGGGAGCTTGGAGGCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 300
 QY 301 GGAGCAGGCAATGTGCAATACCAATCTGTACCTACTGATGCTGTGTAACCACT 360
 DB 301 GGAGCAGGCAATGTGCAATACCAATCTGTACCTACTGATGCTGTGTAACCACT 360
 QY 361 CACAGATTCAGCTTCGGACAGAGACCGCTGTAGACCAAGCCATGCTTTTGAAGT 420
 DB 361 CACAGATTCAGCTTCGGACAGAGACCGCTGTAGACCAAGCCATGCTTTTGAAGT 420
 QY 421 TATTAAGTCTGTGTGGTGCACAAAAGACACTTATCTATGAAGAGGTTCTTTTATC 480
 DB 421 TATTAAGTCTGTGTGGTGCACAAAAGACACTTATCTATGAAGAGGTTCTTTTATC 480
 QY 481 TTGGCCAGTATATGACTTAACGATATATGATGAGAGCAACACATATGATAT 540
 DB 481 TTGGCCAGTATATGACTTAACGATATATGATGAGAGCAACACATATGATAT 540
 QY 541 GTTCAATGATCTTCTAGGAGATTTGTTGGGCTGCGAAGCTTCTGTGGAAGAGCACA 600
 DB 541 GTTCAATGATCTTCTAGGAGATTTGTTGGGCTGCGAAGCTTCTGTGGAAGAGCACA 600
 QY 601 GGAATATATACCATGATCTACAGAACTTGGTGTAGTCAATCAGCAGGAATCATCGG 660
 DB 601 GGAATATATACCATGATCTACAGAACTTGGTGTAGTCAATCAGCAGGAATCATCGG 660
 QY 661 ACTCAGTACATCTGTGAGTGAGACAGCTGCACCTTCAAGGTGGAGTGATCAAAAGG 720
 DB 661 ACTCAGTACATCTGTGAGTGAGACAGCTGCACCTTCAAGGTGGAGTGATCAAAAGG 720

QY 721 ACCTTGTTACAGAGCTTCAGAAAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780
 DB 721 ACCTTGTTACAGAGCTTCAGAAAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780
 QY 781 CTACCTCATCTAGAAAGGAGAGCAATTAGTGAGACAGAAAGAAATTCAGATGATTTATCTG 840
 DB 781 CTACCTCATCTAGAAAGGAGAGCAATTAGTGAGACAGAAAGAAATTCAGATGATTTATCTG 840
 QY 841 GTGACACAAAAGAAAGCGCCACAAATCTGATAGTATTTCCCTTCTCTTTGATGAAGCC 900
 DB 841 GTGACACAAAAGAAAGCGCCACAAATCTGATAGTATTTCCCTTCTCTTTGATGAAGCC 900
 QY 901 TGGCTCTGTCTGTAATAAGGAGATATGTTGCAAGAGAGCAGTACAGTGAATCTACAG 960
 DB 901 TGGCTCTGTCTGTAATAAGGAGATATGTTGCAAGAGAGCAGTACAGTGAATCTACAG 960
 QY 961 GGAGCCCATCGAATCCGGATCTTGTGCTGCTGTAAGTGAACATTCAGGTGATTTGGTGG 1020
 DB 961 GGAGCCCATCGAATCCGGATCTTGTGCTGCTGTAAGTGAACATTCAGGTGATTTGGTGG 1020
 QY 1021 ATCAGGATTCAGTTTTCAGATCAGTTTGTGCTAGCAATTTGAAGTTGAATCTCTCGACTCAG 1080
 DB 1021 ATCAGGATTCAGTTTTCAGATCAGTTTGTGCTAGCAATTTGAAGTTGAATCTCTCGACTCAG 1080
 QY 1081 AAGATTATAGCCTTAGTGAAGAGGAGGAGTATACAGATTCATTTGAAGAGATTCCTGAAA 1140
 DB 1081 AAGATTATAGCCTTAGTGAAGAGGAGGAGTATACAGATTCATTTGAAGAGATTCCTGAAA 1140
 QY 1141 AAGTTACTGTATCAGGAGGAGGAGTATACAGATTCATTTGAAGAGATTCCTGAAA 1200
 DB 1141 AAGTTACTGTATCAGGAGGAGGAGTATACAGATTCATTTGAAGAGATTCCTGAAA 1200
 QY 1201 TTTCTTGTAGTCTGACTATTGGAAATGCATCTCATGCAATGAATGAATCCCTTCTCCAT 1260
 DB 1201 TTTCTTGTAGTCTGACTATTGGAAATGCATCTCATGCAATGAATGAATCCCTTCTCCAT 1260
 QY 1261 CACATTGCAACAGATGTTGGGCGCTTCTGAGAAATTTGGCTTCTGAGATTAAGAGGAAAG 1320
 DB 1261 CACATTGCAACAGATGTTGGGCGCTTCTGAGAAATTTGGCTTCTGAGATTAAGAGGAAAG 1320
 QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAAGAACTCAACACAGCTGAAGAGGCT 1380
 DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAAGAACTCAACACAGCTGAAGAGGCT 1380
 QY 1381 TTGATGTTCTGATTTGTAAGAAACTATAGTGAATGATTTCCAGAGAGTCTGTTGAGG 1440
 DB 1381 TTGATGTTCTGATTTGTAAGAAACTATAGTGAATGATTTCCAGAGAGTCTGTTGAGG 1440
 QY 1441 AAAATGATGATAAAATTAACAAAGCTTCAATCAAGAAAGTGAAGACTATTCTCAGC 1500
 DB 1441 AAAATGATGATAAAATTAACAAAGCTTCAATCAAGAAAGTGAAGACTATTCTCAGC 1500
 QY 1501 CATCAACTTCTAGTAGCATTATTTATAGCAGCCAAAGATGTAAGAGGTTTGAAGGG 1560
 DB 1501 CATCAACTTCTAGTAGCATTATTTATAGCAGCCAAAGATGTAAGAGGTTTGAAGGG 1560
 QY 1561 AAGAAACCCAAAGAAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTGAAC 1620
 DB 1561 AAGAAACCCAAAGAAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTGAAC 1620
 QY 1621 CTTGCTGATTTGTCAAGGTCGACCTTAAATGTTTGCATTTGCCATGGCAAAACAGGAC 1680
 DB 1621 CTTGCTGATTTGTCAAGGTCGACCTTAAATGTTTGCATTTGCCATGGCAAAACAGGAC 1680
 QY 1681 ATCTTATGGCTGCTTTTACATGTGCAAGAGCTAAAGAAAGAAATAAGCCCTGCCAG 1740
 DB 1681 ATCTTATGGCTGCTTTTACATGTGCAAGAGCTAAAGAAAGAAATAAGCCCTGCCAG 1740
 QY 1741 TATCTGACACCAATTCATGTTGCTGCTTACTTATTTCCCTTAGTTCACCTGCTAT 1800
 DB 1741 TATCTGACACCAATTCATGTTGCTGCTTACTTATTTCCCTTAGTTCACCTGCTAT 1800
 QY 1801 AAGAGAAATATATTTTCTAACTATATAACCTAGGAATTTAGACAACTGAAATTTAT 1860

Db 1801 AGAGAAATATATATTTCTACCTATATATACCTTAGGAATTTAGACAACTGAAATTTAT 1860
 Qy 1861 CACATATATCAAAAGTGGAGAAATGCCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
 Db 1861 CACATATATCAAAAGTGGAGAAATGCCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
 Qy 1921 TGACCTACTTTGGTAGTGGATAGTGAATACATACATATATTTGACTTGAATATAGCT 1980
 Db 1921 TGACCTACTTTGGTAGTGGATAGTGAATACATACATATATTTGACTTGAATATAGCT 1980
 Qy 1981 CATCCTTTACCAACTCCCTAAATTTAAATTAATTTCTACTGTCTTAATGAGAAGTAC 2040
 Db 1981 CATCCTTTACCAACTCCCTAAATTTAAATTAATTTCTACTGTCTTAATGAGAAGTAC 2040
 Qy 2041 TTGGTTTTTTTTTTCTTAATATGATATAGACATTTAAATTAATTTCTACTGTCTTAAT 2100
 Db 2041 TTGGTTTTTTTTTTCTTAATATGATATAGACATTTAAATTAATTTCTACTGTCTTAAT 2100
 Qy 2101 AGACCGAGTCTCTGTTTACCCAGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTCTGTTTACCCAGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Qy 2161 AGCTCTGCCCTCCCGGGTTGCGACCATTTCTCTGCTCAGCTCCCAATTAAGCTTGGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTTGCGACCATTTCTCTGCTCAGCTCCCAATTAAGCTTGGCC 2220
 Qy 2221 TACAGTCATCTGCCACACACACCTGGCTAAATTTTGTACTTTTATAGTAGACAGGGTTTC 2280
 Db 2221 TACAGTCATCTGCCACACACACCTGGCTAAATTTTGTACTTTTATAGTAGACAGGGTTTC 2280
 Qy 2281 ACCGTGTTAGCAGGATGGTCTCGATCTCTGACCTCGTGTGCTCGGCCACCTCGGCCCTCC 2340
 Db 2281 ACCGTGTTAGCAGGATGGTCTCGATCTCTGACCTCGTGTGCTCGGCCACCTCGGCCCTCC 2340
 Qy 2341 CAAAGTCTGGGATACAGGCATGAGCCACCG 2372
 Db 2341 CAAAGTCTGGGATACAGGCATGAGCCACCG 2372

RESULT 4

AA166410
 ID AA166410 standard; cDNA; 2372 BP.

XX AC AA166410;

XX 14-SEP-2000 (revised)
 DT 18-JUN-1997 (first entry)

XX Human MDM2 coding sequence.

DE Human; MDM2 protein; antibody; detection; cancer; diagnosis;
 KW p53-regulated growth; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH 312..1787
 FT CDS /*tag= a
 FT /product= MDM2

XX US5618921-A.

XX 08-APR-1997.

XX 07-APR-1992; 92US-0867840.

XX 07-APR-1993; 93US-0044619.

XX 07-APR-1992; 92US-0867840.

XX 23-JUN-1992; 92US-0903103.

XX 17-FEB-1995; 95US-0390479.

XX (UOJO) UNIV JOHNS HOPKINS.

XX Burrell M, Hill DE, Kinzler KW, Vogelstein B;
 PI WPI; 1997-225474/20.
 XX P-PSDB; AAW15463.
 XX Antibodies specific for human MDM2 protein - for diagnosis of cancer
 PT Claim 1; Column 19-24; 35pp; English.
 XX This sequence encodes the human MDM2 protein. Antibodies that
 CC specifically bind to human MDM2 protein may be used for detecting
 CC elevated expression of the MDM2 gene in a human tissue or body
 CC fluid sample, esp. for cancer diagnosis. The antibodies may be used
 CC to interfere with the binding of p53 to MDM2. Elevated levels of MDM2
 CC appear to sequester p53 and allow the cell to escape from p53-regulated
 CC growth.
 CC (N.B. Revised record issued to correct the sequence analysis field.)
 XX Sequence 2372 BP; 598 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 18; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTCCGAAAGATGGA 60
 Db 1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTCCGAAAGATGGA 60
 Qy 61 GCAAGAAGCGAGCCCGAGGGCGCGACCCCTCTGACCGAGATCCTGCTGCTTCG 120
 Db 61 GCAAGAAGCGAGCCCGAGGGCGCGACCCCTCTGACCGAGATCCTGCTGCTTCG 120
 Qy 121 CAGCAGAGAGACCGTCCCTCCCGGATAGTGGTACGAGCGCCAGTCCCTGGCCCG 180
 Db 121 CAGCAGAGAGACCGTCCCTCCCGGATAGTGGTACGAGCGCCAGTCCCTGGCCCG 180
 Qy 181 GAGAGTGAATGATCCCGAGGGCCAGGGCTGCTTCCGAGTAGTCAGTCCCGGTG 240
 Db 181 GAGAGTGAATGATCCCGAGGGCCAGGGCTGCTTCCGAGTAGTCAGTCCCGGTG 240
 Qy 241 AAGGAACTGGGAGTCTTGGAGGACCCCGACCTCCAAAGCGGAAACCCCGGATGGA 300
 Db 241 AAGGAACTGGGAGTCTTGGAGGACCCCGACCTCCAAAGCGGAAACCCCGGATGGA 300
 Qy 301 GGAGCGCAAACTGCAATACCAACATGCTGTACTACTGTGTTGCTGTTGCTGTTGCT 360
 Db 301 GGAGCGCAAACTGCAATACCAACATGCTGTACTACTGTGTTGCTGTTGCTGTTGCT 360
 Qy 361 CACAGATTCAGCTTCGGAACAGAGACCCCTGGTTAGACCAAGCCATTCCTTTGAAGT 420
 Db 361 CACAGATTCAGCTTCGGAACAGAGACCCCTGGTTAGACCAAGCCATTCCTTTGAAGT 420
 Qy 421 TATTAAAGTCTGTTGGTGACAAAAAGACACTTATATCTATGAAAGAGTCTTTTATC 480
 Db 421 TATTAAAGTCTGTTGGTGACAAAAAGACACTTATATCTATGAAAGAGTCTTTTATC 480
 Qy 481 TTGGCCAGTATATGACTAAACGATTATATGATGAGAGCAACACATATGTTATTT 540
 Db 481 TTGGCCAGTATATGACTAAACGATTATATGATGAGAGCAACACATATGTTATTT 540
 Qy 541 GTTCAAAATGATCTTCTAGGAGATTGTTGGCGTGCCCAAGCTTCTCTGTGAAGAGCACA 600
 Db 541 GTTCAAAATGATCTTCTAGGAGATTGTTGGCGTGCCCAAGCTTCTCTGTGAAGAGCACA 600
 Qy 601 GGAAATATATACCATGATCTACAGGAACCTGGTAGTAGCAATCAGCAGGAATCATCGG 660
 Db 601 GGAAATATATACCATGATCTACAGGAACCTGGTAGTAGCAATCAGCAGGAATCATCGG 660
 Qy 661 ACTCAGGTACATCTGTCAGTGGAGAACAGGTCACCTTGAAGGTGGAGTGATCAAAAGG 720
 Db 661 ACTCAGGTACATCTGTCAGTGGAGAACAGGTCACCTTGAAGGTGGAGTGATCAAAAGG 720

QY 721 ACCTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780
 DB 721 ACCTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780
 QY 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTCG 840
 DB 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTCG 840
 QY 841 GTGAACGACAAAGAAAACGCCCAAAATCTGATAGTATTTCCCTTTTCTTTGATGAAGCC 900
 DB 841 GTGAACGACAAAGAAAACGCCCAAAATCTGATAGTATTTCCCTTTTCTTTGATGAAGCC 900
 QY 901 TGGCTCTGTGTATTAAGGGAGATATGTTGTGAAGAAGACAGTACAGTGAATCTACAG 960
 DB 901 TGGCTCTGTGTATTAAGGGAGATATGTTGTGAAGAAGACAGTACAGTGAATCTACAG 960
 QY 961 GGACGCCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATTTGGTTGG 1020
 DB 961 GGACGCCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATTTGGTTGG 1020
 QY 1021 ATCAGGATTCAGTTTCAGATCAGTTAGTGTAGATTTGAATTTGAATCTTCGACTCAG 1080
 DB 1021 ATCAGGATTCAGTTTCAGATCAGTTAGTGTAGATTTGAATTTGAATCTTCGACTCAG 1080
 QY 1081 AAGATTATAGCTTAGTGAAGAGGACAAAGTCTCAGATGAAGTATGATGAGGTATATC 1140
 DB 1081 AAGATTATAGCTTAGTGAAGAGGACAAAGTCTCAGATGAAGTATGATGAGGTATATC 1140
 QY 1141 AAGTTACTGTATCAGCGAGGGAGAGTATACAGATTCATTTGAAGAAGATCCTGAA 1200
 DB 1141 AAGTTACTGTATCAGCGAGGGAGAGTATACAGATTCATTTGAAGAAGATCCTGAA 1200
 QY 1201 TTTCTTACGTGACTTATTTGAAGTGCATCTCATGCAATGAATGAATCCCTCCCTTCCAT 1260
 DB 1201 TTTCTTACGTGACTTATTTGAAGTGCATCTCATGCAATGAATGAATCCCTCCCTTCCAT 1260
 QY 1261 CACATTCGACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCCTGAGATGAAGGAAAG 1320
 DB 1261 CACATTCGACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCCTGAGATGAAGGAAAG 1320
 QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAGCTGAAGAGGGCT 1380
 DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAGCTGAAGAGGGCT 1380
 QY 1381 TTGATGTTCTCGATTTGTAAGAAACTATAGTGAATGATCCAGAGAGTCAATGTTGAGG 1440
 DB 1381 TTGATGTTCTCGATTTGTAAGAAACTATAGTGAATGATCCAGAGAGTCAATGTTGAGG 1440
 QY 1441 AAAATGATGATTAATAATACAGAACTTCAATCACAAGAAAGTGAAGACTATTTCTCAGC 1500
 DB 1441 AAAATGATGATTAATAATACAGAACTTCAATCACAAGAAAGTGAAGACTATTTCTCAGC 1500
 QY 1501 CATCAACTCTCTAGTAGCATTTATTTATAGCAGCCCAAGAGATGTAAGAGTGTGAAAGGG 1560
 DB 1501 CATCAACTCTCTAGTAGCATTTATTTATAGCAGCCCAAGAGATGTAAGAGTGTGAAAGGG 1560
 QY 1561 AAGAAACCCAGACAAAGAGAGTGTGNAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
 DB 1561 AAGAAACCCAGACAAAGAGAGTGTGNAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
 QY 1621 CTTGTGTGATTTGTCAAGGTCGACCTAAAATGTTTGCATTTGCTGATGCGCAAAACAGGAC 1680
 DB 1621 CTTGTGTGATTTGTCAAGGTCGACCTAAAATGTTTGCATTTGCTGATGCGCAAAACAGGAC 1680
 QY 1681 ATCTTATGGCTGCTTTACATGTCGAAGAAGCTTAAGAAGAAAGGAATTAAGCCCTGCCAG 1740
 DB 1681 ATCTTATGGCTGCTTTACATGTCGAAGAAGCTTAAGAAGAAAGGAATTAAGCCCTGCCAG 1740
 QY 1741 TATGTAGACAAACCAATTCAAATGATTTGCTGAATCTTTTCCCTTCTAGTGTGACCTGTCTAT 1800
 DB 1741 TATGTAGACAAACCAATTCAAATGATTTGCTGAATCTTTTCCCTTCTAGTGTGACCTGTCTAT 1800
 QY 1801 AAGAGAAATATATTTCTTAACTATATAACCCCTAGGAATTTAGACAAACCTGAAATTTATT 1860

DB 1801 AAGAGAAATATATTTCTTAACTATATAACCCCTAGGAATTTAGACAAACCTGAAATTTATT 1860
 QY 1861 CACATATATCAAAAGTGAAGAAATCCCTCAATTCACATAGATTTCTCTCTCTTTAGTATAAT 1920
 DB 1861 CACATATATCAAAAGTGAAGAAATCCCTCAATTCACATAGATTTCTCTCTCTTTAGTATAAT 1920
 QY 1921 TGACCTACTTTGGTAGGGAATAGTGAATCTTACTTATTAATTTGACTTGAATATGTAGCT 1980
 DB 1921 TGACCTACTTTGGTAGGGAATAGTGAATCTTACTTATTAATTTGACTTGAATATGTAGCT 1980
 QY 1981 CATCTTTTACACCAACTCCCTAAATTTAAATTAATTTCTACTCTCTCTTAATGAGAAGTAC 2040
 DB 1981 CATCTTTTACACCAACTCCCTAAATTTAAATTAATTTCTACTCTCTCTTAATGAGAAGTAC 2040
 QY 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTG 2100
 DB 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTG 2100
 QY 2101 AGACCGAGTCTTGCTCTGTTTACCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 DB 2101 AGACCGAGTCTTGCTCTGTTTACCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 QY 2161 AGCTCTGCCCTCCCGGGTTGCGACCAATTCCTGCTCAGCCTCCCAATAGCTTTGGCC 2220
 DB 2161 AGCTCTGCCCTCCCGGGTTGCGACCAATTCCTGCTCAGCCTCCCAATAGCTTTGGCC 2220
 QY 2221 TACAGTCACTGCGCCACACACACCTGGCTAAATTTTGTACTTTTAGTAGACAGGCTTTC 2280
 DB 2221 TACAGTCACTGCGCCACACACACCTGGCTAAATTTTGTACTTTTAGTAGACAGGCTTTC 2280
 QY 2281 ACCGTGTTAGCAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGGCTCC 2340
 DB 2281 ACCGTGTTAGCAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGGCTCC 2340
 QY 2341 CAAAGTCTGGGATTACAGGCATGAGCCCG 2372
 DB 2341 CAAAGTCTGGGATTACAGGCATGAGCCCG 2372

RESULT 5
 AAT62065
 ID AAT62065 standard; cDNA; 2372 BP.
 XX
 AC AAT62065;
 DT 05-JUN-1997 (first entry)
 XX
 DE Human MDM2 cDNA.
 XX
 KW Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection;
 KW amplification; elevation; expression; diagnosis; neoplasia;
 KW neoplastic transformation; sarcoma; colorectal; lung cancer;
 KW chronic myelogenous leukaemia; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 312..1787
 FT /*tag= a
 FT /product= MDM2
 FT
 FT US5606044-A.
 PN
 XX 25-FEB-1997.
 PD
 XX 07-APR-1992; 92US-0867840.
 XX
 PR 07-APR-1993; 93US-0044619.
 PR 07-APR-1992; 92US-0867840.
 PR 23-JUN-1992; 92US-0903103.
 PR 17-FEB-1995; 95US-0390546.
 XX

QY 1801 AAGAGAAATTAATATTTCTAACTATATTAACCTAGGAATTTAGACAACTGAAATTTATT 1860
 Db 1801 AAGAGAAATTAATATTTCTAACTATATTAACCTAGGAATTTAGACAACTGAAATTTATT 1860
 QY 1861 CACATATATCAAAAGTGGAGAAATGCTCAATTCACATAGATTTCTCTTTAGTATAAT 1920
 Db 1861 CACATATATCAAAAGTGGAGAAATGCTCAATTCACATAGATTTCTCTTTAGTATAAT 1920
 QY 1921 TGACCTACTTTGGTAGTGAATAGTAACTACTATATAATTTGACTTGAATATGAGCT 1980
 Db 1921 TGACCTACTTTGGTAGTGAATAGTAACTACTATATAATTTGACTTGAATATGAGCT 1980
 QY 1981 CATCTTTACACCAACTCCTAAATTTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 Db 1981 CATCTTTACACCAACTCCTAAATTTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 QY 2041 TTGGCTTTTCTTCTTAAATATGATATGACATTTAAATGTAATTAATTTATTTTGTG 2100
 Db 2041 TTGGCTTTTCTTCTTAAATATGATATGACATTTAAATGTAATTAATTTATTTTGTG 2100
 QY 2101 AGACCGAGTCTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGCTCACTGCA 2160
 QY 2161 AGCTCTGCCCTCCCGGTTCCGACCATCTCTGCTCAGCTCCCAATTAGCTTGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGTTCCGACCATCTCTGCTCAGCTCCCAATTAGCTTGCC 2220
 QY 2221 TACAGTCTGCCACACACCTGGCTAAATTTTGTACTTTAGTAGACAGGGTTTC 2280
 Db 2221 TACAGTCTGCCACACACCTGGCTAAATTTTGTACTTTAGTAGACAGGGTTTC 2280
 QY 2281 ACCGTGTAGCAGGATGTCGTGATCTCTGACCTCTGTGATCCGCCACCTCGCCCTCC 2340
 Db 2281 ACCGTGTAGCAGGATGTCGTGATCTCTGACCTCTGTGATCCGCCACCTCGCCCTCC 2340
 QY 2341 CAAAGTCTGGGATTACAGCATGAGCCACCG 2372
 Db 2341 CAAAGTCTGGGATTACAGCATGAGCCACCG 2372

RESULT 6
 AAV28876
 ID AAV28876 standard; cDNA; 2372 BP.
 XX
 AC AAV28876;
 XX
 DE Human MDM2 gene.
 XX
 KW Human; p53; MDM2; tumour; growth inhibition; amplification;
 KW malignant fibrous histiocytoma; liposarcoma; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 312..1787
 FT /*tag= a
 FT /product= "MDM2 protein"
 XX
 PN US5756455-A,
 XX
 PD 26-MAY-1998.
 XX
 PF 17-FEB-1995; 9505-0390515.
 XX
 PR 07-APR-1993; 9305-004619.
 PR 07-APR-1992; 9205-0867840.
 PR 23-JUN-1992; 9205-0903103.
 PR 17-FEB-1995; 9505-0390515.
 XX

(UYJO) UNIV JOHNS HOPKINS.
 XX Kinzler KW, Vogelstein B;
 XX WPI; 1998-321574/28.
 DR P-PSDB; AAW57241.
 XX
 PT Inhibiting growth of tumour cells having MDM2 gene amplification -
 PT with p53 protein fragment
 XX
 PS Example 1; Column 19-24; 40pp; English.
 XX
 CC A method has been developed for inhibiting the growth of tumour cells
 CC containing a human MDM2 gene amplification. The method comprises
 CC treating the tumour cells with a DNA molecule that expresses a
 CC polypeptide capable of binding to human MDM2 protein. The present
 CC sequence represents the human MDM2 gene. The present invention describes
 CC three preferred polypeptides for binding human MDM2: (1) the polypeptide
 CC comprises amino acids 1-50 of p53 (see AAW57240); (2) the polypeptide
 CC comprises amino acids 13-41 of p53 (see AAW57240) and at least none
 CC additional p53 residues on the N- or C-terminal side, provided that the
 CC polypeptide lacks the homooligomerisation domain of p53; (3) the
 CC polypeptide comprises amino acids 13-41 of p53 (see AAW57241) and at
 CC least nine additional p53 residues on the N- or C-terminal side, provided
 CC that the polypeptide lacks amino acids 138-393 of p53. Some malignant
 CC fibrous histiocytomas and liposarcomas have an MDM2 gene amplification,
 CC so detection of increased expression of MDM2 gene products indicates
 CC tumorigenesis.
 XX
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
 Query Match 100.0%; Score 2372; DB 19; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCACCGCGCGAGCTTGGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 Db 1 GCACCGCGCGAGCTTGGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 QY 61 GCAAGAAAGCGAGCGCGGAGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 Db 61 GCAAGAAAGCGAGCGCGGAGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 QY 121 CAGCCAGGAGCGACCGCTCCCTCCCGGATGAGTGGTACGAGCGCGGCGGCGGCGGCGGCGG 180
 Db 121 CAGCCAGGAGCGACCGCTCCCTCCCGGATGAGTGGTACGAGCGCGGCGGCGGCGGCGGCGG 180
 QY 181 GAGAGTGAATGATCCCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 Db 181 GAGAGTGAATGATCCCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 QY 241 AAGGAAACTGGGAGTCTTCGAGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 Db 241 AAGGAAACTGGGAGTCTTCGAGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 QY 301 GGAGCGCAAAATGTGCAATACCAACATGTCTGTACTACTGTGTGTGTGTGTGTGTGTGTGT 360
 Db 301 GGAGCGCAAAATGTGCAATACCAACATGTCTGTACTACTGTGTGTGTGTGTGTGTGTGTGT 360
 QY 361 CACAGATTCCAGCTTCGGAACAAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 Db 361 CACAGATTCCAGCTTCGGAACAAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 QY 421 TATTAAGTCTGTTGGTGCACAAAAGACACTTATATGATGAGAGGTTCTTTTATC 480
 Db 421 TATTAAGTCTGTTGGTGCACAAAAGACACTTATATGATGAGAGGTTCTTTTATC 480
 QY 481 TTGGCCAGTATATTGACTAAACGATTTATGATGAGAGCAACCAACATATTGTATATT 540
 Db 481 TTGGCCAGTATATTGACTAAACGATTTATGATGAGAGCAACCAACATATTGTATATT 540
 QY 541 GTTCAATGATCTTCTAGGAGATTGTTGGGCGTCCCAAGCTTCTCTGTGAAAGAGCACA 600
 Db 541 GTTCAATGATCTTCTAGGAGATTGTTGGGCGTCCCAAGCTTCTCTGTGAAAGAGCACA 600

Db	541	GTTCAAATGANTCTTAGAGAGATTGTTGGGGTGCCCAAGCTTCTCTGTGTAAGAGAGACA	600
Qy	601	GGAAATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAGCAGGAATCATCGG	660
Db	601	GGAAATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAGCAGGAATCATCGG	660
Qy	661	ACTCAGGTACATCTGTGAGTGAGACAGGTGTCACTTGAAGGTGGAGGTGATCAAAAGG	720
Db	661	ACTCAGGTACATCTGTGAGTGAGACAGGTGTCACTTGAAGGTGGAGGTGATCAAAAGG	720
Qy	721	ACCTTGTACAAGAGCTTCAGGAAGAAACCTTCACTTTCACATTTTGGTTCTAGACCAT	780
Db	721	ACCTTGTACAAGAGCTTCAGGAAGAAACCTTCACTTTCACATTTTGGTTCTAGACCAT	780
Qy	781	CTACCTCATCTAGAAGGAGCAATTAGTGACAGAGAAGAAATTCAGATGAATATCTG	840
Db	781	CTACCTCATCTAGAAGGAGCAATTAGTGACAGAGAAGAAATTCAGATGAATATCTG	840
Qy	841	GTGAAGCACAAGAAAGCCCAAAATCTGATAGTATTTCCCTTTCCTTTGATGAAGCC	900
Db	841	GTGAAGCACAAGAAAGCCCAAAATCTGATAGTATTTCCCTTTCCTTTGATGAAGCC	900
Qy	901	TGSCCTCTGTGTAAATGAAGGAGATGTGTGTGAAGAAAGCAGTAGCAGTGAATCTACAG	960
Db	901	TGSCCTCTGTGTAAATGAAGGAGATGTGTGTGAAGAAAGCAGTAGCAGTGAATCTACAG	960
Qy	961	GGACGCCATCGAATCCGGATCTTGATGCTGTGTGAAGTGAACATTCAGGTGATGGTTGG	1020
Db	961	GGACGCCATCGAATCCGGATCTTGATGCTGTGTGAAGTGAACATTCAGGTGATGGTTGG	1020
Qy	1021	ATCAGGATTCAGTTTCAGATCAGTTTAGTGTAGAAATTTGAAGTTGAATCTCTCGACTCAG	1080
Db	1021	ATCAGGATTCAGTTTCAGATCAGTTTAGTGTAGAAATTTGAAGTTGAATCTCTCGACTCAG	1080
Qy	1081	AGATATATAGCCTTAGTGAAGAACCAAGAACTCTCAGATGAAGATGATGAGGTATATC	1140
Db	1081	AGATATATAGCCTTAGTGAAGAACCAAGAACTCTCAGATGAAGATGATGAGGTATATC	1140
Qy	1141	AAGTTACTGTGTATCAGGCAGGGAGAGTGTATACAGATTCATTTGAAGAAGACTCTCGAAA	1200
Db	1141	AAGTTACTGTGTATCAGGCAGGGAGAGTGTATACAGATTCATTTGAAGAAGACTCTCGAAA	1200
Qy	1201	TTTCCCTTACTGACTATTCGAATCGCTTCATCGAATGAATCAATCAATCCCTTCCAT	1260
Db	1201	TTTCCCTTACTGACTATTCGAATCGCTTCATCGAATGAATCAATCAATCCCTTCCAT	1260
Qy	1261	CACATTCGAACAGATTTGGGCCCTTCGTGGAATTTGGCTTCCTGAAGATTAAGGGGAAG	1320
Db	1261	CACATTCGAACAGATTTGGGCCCTTCGTGGAATTTGGCTTCCTGAAGATTAAGGGGAAG	1320
Qy	1321	ATAAGGGGAATCTCTGAGAAGCCAACTGGAAACTCAACACAGCTGAAGAGGCT	1380
Db	1321	ATAAGGGGAATCTCTGAGAAGCCAACTGGAAACTCAACACAGCTGAAGAGGCT	1380
Qy	1381	TTGATGTTCTGATGTGTAATAAACTATAGTGAATTTCCAGAGAGTCAATGTTGAGG	1440
Db	1381	TTGATGTTCTGATGTGTAATAAACTATAGTGAATTTCCAGAGAGTCAATGTTGAGG	1440
Qy	1441	AAAATGATGATAAATTTACACAGCTTCACATCAACAAGAAGTGAAGACTATTTCTCAGC	1500
Db	1441	AAAATGATGATAAATTTACACAGCTTCACATCAACAAGAAGTGAAGACTATTTCTCAGC	1500
Qy	1501	CATCAACTTCTAGTAGCATTTATATAGCAGCCAAGAGATGTGAAAGAGTTTGAAGAGG	1560
Db	1501	CATCAACTTCTAGTAGCATTTATATAGCAGCCAAGAGATGTGAAAGAGTTTGAAGAGG	1560
Qy	1561	AAGAAACCCAAAGACAAGAGAGAGTGTGGAATCTAGTTTCCCTTAAATGCCATTTGAAC	1620
Db	1561	AAGAAACCCAAAGACAAGAGAGAGTGTGGAATCTAGTTTCCCTTAAATGCCATTTGAAC	1620
Qy	1621	CTTGTGTGATTTGTCAAGTTCGACCTTAAATAATGGTTGCATTTGCCATGCGCAAAACAGGAC	1680
Db	1621	CTTGTGTGATTTGTCAAGTTCGACCTTAAATAATGGTTGCATTTGCCATGCGCAAAACAGGAC	1680

Qy	1681	ATCTTATGGCGCTGCTTTACATGTGCMAAGAAGCTAAAGAAAGAGTAATAGCCCTCGCCACG	1740
Db	1681	ATCTTATGGCGCTGCTTTACATGTGCMAAGAAGCTAAAGAAAGAGTAATAGCCCTCGCCACG	1740
Qy	1741	TATGTAGACACCAAAATTCAAATGATTTGTCTAACTTATTTCCCTTAGTGTACCTGTGTAT	1800
Db	1741	TATGTAGACACCAAAATTCAAATGATTTGTCTAACTTATTTCCCTTAGTGTACCTGTGTAT	1800
Qy	1801	AAGAGAAATTAATATTTCTAACTATATAACCCCTAGGAATTTAGACAACCTGAAATTTATT	1860
Db	1801	AAGAGAAATTAATATTTCTAACTATATAACCCCTAGGAATTTAGACAACCTGAAATTTATT	1860
Qy	1861	CACATATATCAAAAGTGAGAAAATGGCTCAAAATTCACATAGATTTCTTCTCTTAGTATAAT	1920
Db	1861	CACATATATCAAAAGTGAGAAAATGGCTCAAAATTCACATAGATTTCTTCTCTTAGTATAAT	1920
Qy	1921	TGACCTACTTTGGTAGTGGAAATAGTGAATACTTACTATAAATTTGACTTTGAATATGTAGCT	1980
Db	1921	TGACCTACTTTGGTAGTGGNAATAGTGAATACTTACTATAAATTTGACTTTGAATATGTAGCT	1980
Qy	1981	CATCCTTTACACCAACTCTTAATTTTAAATAATTTCTACTCTGTCTTAAATGAGAAATAC	2040
Db	1981	CATCCTTTACACCAACTCTTAATTTTAAATAATTTCTACTCTGTCTTAAATGAGAAATAC	2040
Qy	2041	TTGGTTTTTTTTTTCTTAAATATGATATGACATTAATAATGTAACCTATTATTTTTTTTG	2100
Db	2041	TTGGTTTTTTTTTTTCTTAAATATGATATGACATTAATAATGTAACCTATTATTTTTTTTG	2100
Qy	2101	AGACCGAGTCTTCTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACATGCA	2160
Db	2101	AGACCGAGTCTTCTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACATGCA	2160
Qy	2161	AGCTCTGCCCTCCCGGGTTGCGACCATTTCTCCTGCCTACGCTCCCAATTTAGCTTGCC	2220
Db	2161	AGCTCTGCCCTCCCGGGTTGCGACCATTTCTCCTGCCTACGCTCCCAATTTAGCTTGCC	2220
Qy	2221	TACAGTCTATCTGCCACACACACCTTGGCTAAATTTTGTACTTTTAGTAGACACAGGGTTTC	2280
Db	2221	TACAGTCTATCTGCCACACACACCTTGGCTAAATTTTGTACTTTTAGTAGACACAGGGTTTC	2280
Qy	2281	ACCGTGTACCGAGATGTTCTGATCTCCTGACCTCTGTGATCGCCGCCACCTCGGCCCTCC	2340
Db	2281	ACCGTGTGTAGCCAGATGGTCTCGATCTCCTGACCTCTGTGATCGCCGCCACCTCGGCCCTCC	2340
Qy	2341	CAAAAGTCTGGGATTAACAGGCATGAGCCACCG	2372
Db	2341	CAAAAGTCTGGGATTAACAGGCATGAGCCACCG	2372

RESULT 7	
AAV20549	
ID	AAV20549 standard; cDNA; 2372 BP.
XX	
AC	AAV20549;
XX	
DT	18-JUN-1998 (first entry)
XX	
DE	Human MDM2 encoding cDNA.
XX	
KW	Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;
KW	sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma; sarcoma; ss
XX	
OS	Homo sapiens.
XX	
PH	
FT	Key
FT	312..1787
FT	/*tag= a
FT	/product= "MDM2"
XX	
PN	
XX	US5736338-A.
XX	
PD	07-APR-1998.

XX PF 17-FEB-1995; 95US-0390517.
XX PR 07-APR-1993; 93US-0044619.
XX PR 07-APR-1992; 92US-0867840.
XX PR 23-JUN-1992; 92US-0903103.
XX PR 17-FEB-1995; 95US-0390517.
XX PA (UVOJ) UNIV JOHNS HOPKINS.
XX PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;
XX DR WPT; 1998-239206/21.
XX DR P-PSDB; NAW48241.
XX PT Cancer diagnosis - by determination of MDM2 protein
XX PS Claim 1; Column 21-24; 35pp; English.
XX CC The present sequence encodes human MDM2 (hMDM2) which is used in the
CC method of the present invention. The present invention describes a
CC method for diagnosing a neoplastic disease caused by overexpression
CC of MDM2 protein. The method comprises detecting an elevated cellular
CC amount of this protein. The method is useful for the diagnosis of
CC sarcoma, especially liposarcoma, malignant fibrous histiocytoma or
CC osteosarcoma.
XX CC
XX SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 19; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCAGCTTGGCTGCTCTCTGGGCCCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
DB 1 GCACCGCGCAGCTTGGCTGCTCTCTGGGCCCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60

QY 61 GCAGAAGCGCGCGAGGGGGCGCGGACCCCTCTGACGGAGATCTGCTGCTTTCG 120
DB 61 GCAAGAAGCGCGCGAGGGGGCGCGGACCCCTCTGACGGAGATCTGCTGCTTTCG 120

QY 121 CAGCCAGGAGCAGCTCCCTCCCGGATTAGTGTGCTAGGAGCGGCCGCTGGCCCG 180
DB 121 CAGCCAGGAGCAGCTCCCTCCCGGATTAGTGTGCTAGGAGCGGCCGCTGGCCCG 180

QY 181 GAGAGTGAATGATCCCGAGCGCCAGGCGCTGCTTCCGAGTAGTCACTCCCGTG 240
DB 181 GAGAGTGAATGATCCCGAGCGCCAGGCGCTGCTTCCGAGTAGTCACTCCCGTG 240

QY 241 AAGGAAACTGGGAGTCTTTGAGGGACCCCGGACTCCAGCGCGAAACCCCGGATGGA 300
DB 241 AAGGAAACTGGGAGTCTTTGAGGGACCCCGGACTCCAGCGCGAAACCCCGGATGGA 300

QY 301 GGACGAGCAATGTGCAATACCAATCTGTACCTACTGATGGTCTGTACCACT 360
DB 301 GGACGAGCAATGTGCAATACCAATCTGTACCTACTGATGGTCTGTACCACT 360

QY 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATGCTTTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATGCTTTTGAAGT 420

QY 421 TATTAAAGTCTGTTGGTGCAAAAAGACACTTATATCTATGAAAGAGTCTTTTATC 480
DB 421 TATTAAAGTCTGTTGGTGCAAAAAGACACTTATATCTATGAAAGAGTCTTTTATC 480

QY 481 TTGGCCAGTATATATGACTAAACGATTATATGATGAGAGCAACATATTGTATT 540
DB 481 TTGGCCAGTATATATGACTAAACGATTATATGATGAGAGCAACATATTGTATT 540

QY 541 GTTCAAAATGATCTTCTAGGAGATTGTTGGCGTGCAGGCTTCTCTGTGAACAGCACA 600
DB 541 GTTCAAAATGATCTTCTAGGAGATTGTTGGCGTGCAGGCTTCTCTGTGAACAGCACA 600

QY 601 GGAAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
DB 601 GGAAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660

QY 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTCACCTTTGAAGGTGGGAGTGATCAAAAGG 720
DB 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTCACCTTTGAAGGTGGGAGTGATCAAAAGG 720

QY 721 ACCTTGTACAGAGCTTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780
DB 721 ACCTTGTACAGAGCTTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780

QY 781 CTACCTCATCTAGAAGAGAGCAATTTAGTGAGACAGAGAAATAATTCAGATGAATTTCTG 840
DB 781 CTACCTCATCTAGAAGAGAGCAATTTAGTGAGACAGAGAAATAATTCAGATGAATTTCTG 840

QY 841 GTGAACGACAAAGAAACGCCACAAATCTGATAGTATTTCCCTTTCCTTTGATGAAAGCC 900
DB 841 GTGAACGACAAAGAAACGCCACAAATCTGATAGTATTTCCCTTTCCTTTGATGAAAGCC 900

QY 901 TGGCTCTGTGTGTAATAAGGGAGATATTTGTGAAAGAGCAGTAGCAGTGAATTTCTACAG 960
DB 901 TGGCTCTGTGTGTAATAAGGGAGATATTTGTGAAAGAGCAGTAGCAGTGAATTTCTACAG 960

QY 961 GGAGCCCATCGAATCCGGATCTTGATGCTGTGTGTAAGTGAACATTCAGGTGATTTGGTGG 1020
DB 961 GGAGCCCATCGAATCCGGATCTTGATGCTGTGTGTAAGTGAACATTCAGGTGATTTGGTGG 1020

QY 1021 ATCAGGATTCAGTTTTCAGATCAGTTTGTAGTGTAGAAATTTGAAAGTGTCTCTGACATCAG 1080
DB 1021 ATCAGGATTCAGTTTTCAGATCAGTTTGTAGTGTAGAAATTTGAAAGTGTCTCTGACATCAG 1080

QY 1081 AAGATTATAGCCTTAGTGAAGAGGACAAAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
DB 1081 AAGATTATAGCCTTAGTGAAGAGGACAAAGAACTCTCAGATGAAGATGATGAGGTATATC 1140

QY 1141 AAGTTACTGTGTATCAGGCGAGGAGAGTATACAGATTCATTTGAAGAGATCCTGAAA 1200
DB 1141 AAGTTACTGTGTATCAGGCGAGGAGAGTATACAGATTCATTTGAAGAGATCCTGAAA 1200

QY 1201 TTTCTTGTAGTCTACTATTGGAATGCACTTCATGCAATGAAATGAATCCCTCCCTTCCAT 1260
DB 1201 TTTCTTGTAGTCTACTATTGGAATGCACTTCATGCAATGAAATGAATCCCTCCCTTCCAT 1260

QY 1261 CACATTCGACAGATGTTGGCCCTTCTGAGAAATGAGTGGCTTCTCCTCAAGATAAAGGAAAG 1320
DB 1261 CACATTCGACAGATGTTGGCCCTTCTGAGAAATGAGTGGCTTCTCCTCAAGATAAAGGAAAG 1320

QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACAGCTGAAGAGGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACAGCTGAAGAGGGCT 1380

QY 1381 TTGATGTTCTGATTTGTAATAAAGTATAGTCAATGATTCAGAGAGTCACTGCTTGGG 1440
DB 1381 TTGATGTTCTGATTTGTAATAAAGTATAGTCAATGATTCAGAGAGTCACTGCTTGGG 1440

QY 1441 AAAATGATGATAAAATTTACAAAGCTTCAAACTCAAGAAAGTGAAGACTATTTCTCAGC 1500
DB 1441 AAAATGATGATAAAATTTACAAAGCTTCAAACTCAAGAAAGTGAAGACTATTTCTCAGC 1500

QY 1501 CATCAACTTCTAGTAGCATTTATTTATAGCAGCCAAAGAGATGTGAAGAGTTTCTGAAGGG 1560
DB 1501 CATCAACTTCTAGTAGCATTTATTTATAGCAGCCAAAGAGATGTGAAGAGTTTCTGAAGGG 1560

QY 1561 AAGAAACCCAGACAAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAAATGCCATTTGAAC 1620
DB 1561 AAGAAACCCAGACAAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAAATGCCATTTGAAC 1620

QY 1621 CTTCTGTGATTGTGTAAGGTCGACCTTAAAAATGGTTGCAATTCCTCCATGCGCAAAACAGCAG 1680
DB 1621 CTTCTGTGATTGTGTAAGGTCGACCTTAAAAATGGTTGCAATTCCTCCATGCGCAAAACAGCAG 1680

QY 1681 ATCTTATGGCCCTGCTTTTACATGTGCAAGAGACTAAAGAAAGGAATAAGCCCTGCCACG 1740

1681 ATCTTATGCGCTGCTTTACATGTGCAAGAGAGCTTAAAGAAAGAAATAGCCCTGCCCCAG 1740
 QY 1741 TATGTAGACAAACCAATCAAAATGATGTGCTTAACCTTATTTCCCTAGTTGACCTGCTAT 1800
 Db 1741 TATGTAGACAAACCAATCAAAATGATGTGCTTAACCTTATTTCCCTAGTTGACCTGCTAT 1800
 QY 1801 AAGAGAAATATATATTTCTAACTATATAACCCCTAGGAATTTAGACAACTGAAATTTAT 1860
 Db 1801 AAGAGAAATATATATTTCTAACTATATAACCCCTAGGAATTTAGACAACTGAAATTTAT 1860
 QY 1861 CACATATATCAAGAGAGAAATGCTCAATTCACATAGATTTCTTCTCTTTAGTATAT 1920
 Db 1861 CACATATATCAAGAGAGAAATGCTCAATTCACATAGATTTCTTCTCTTTAGTATAT 1920
 QY 1921 TGACCTACTTTGGTAGTGGAAATAGTAATCTTACTATAATTTGACTTGAATATGAGCT 1980
 Db 1921 TGACCTACTTTGGTAGTGGAAATAGTAATCTTACTATAATTTGACTTGAATATGAGCT 1980
 QY 1981 CATCCTTTACCAACTCCTTAATTTTAAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 Db 1981 CATCCTTTACCAACTCCTTAATTTTAAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 QY 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTATTTATTTTGTG 2100
 Db 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTATTTATTTTGTG 2100
 QY 2101 AGACCGAGTCTTGTCTGTACCCAGGCTGGAGTGCAGTGGCTGATCTTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTTGTCTGTACCCAGGCTGGAGTGCAGTGGCTGATCTTGGCTCACTGCA 2160
 QY 2161 AGCTCTGCGCTCCCGGGTGTGACCAATCTCTGCTCTGACCTCCCAATGACTTGGCC 2220
 Db 2161 AGCTCTGCGCTCCCGGGTGTGACCAATCTCTGCTCTGACCTCCCAATGACTTGGCC 2220
 QY 2221 TACAGTCATCTGCCACCACTGCTCAATTTTGTACTTTTGTAGTAGACAGGCTTTC 2280
 Db 2221 TACAGTCATCTGCCACCACTGCTCAATTTTGTACTTTTGTAGTAGACAGGCTTTC 2280
 QY 2281 ACCGTTTACGAGAGTGTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCT 2340
 Db 2281 ACCGTTTACGAGAGTGTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCT 2340
 QY 2341 CAAAGTGCTGGGATACAGGATGAGCCACCG 2372
 Db 2341 CAAAGTGCTGGGATACAGGATGAGCCACCG 2372

RESULT 8
 AAV04836
 ID AAV04836 standard; cDNA; 2372 BP.

AC AAV04836;
 AC AAV04836;
 DT 30-APR-1998 (first entry)
 XX cDNA sequence of human MDM2.

MDM2; tumour; diagnosis; neoplasia; DNA binding protein;
 p53 polypeptide; binding; tumour cell; p53-regulated growth;
 inhibition; anti-cancer agent; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 312..1787
 FT /*tag= a

XX US5708136-A.
 PN 13-JAN-1998.

XX 17-FEB-1995; 95US-0390516.

XX 07-APR-1993; 93US-0044619.
 PR 07-APR-1992; 92US-0867840.
 PR 23-JUN-1992; 92US-0903103.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Burrell M, Hill DE, Kinzler KW, Vogelstein B;
 XX WPI; 1998-100408/09.
 PT Human MDM2 binding polypeptide - comprises fragments of p53, useful
 PT in re-establishing p53-regulated growth control in cells
 PT over-expressing MDM2
 XX Disclosure; Columns 19-24; 41pp; English.
 CC The present sequence encodes human MDM2. The MDM2 gene is amplified in
 CC some human tumours. The amplification of this gene is diagnostic of
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a
 CC potential DNA binding protein that functions in the modulation of
 CC expression of other genes and, when present in excess, interferes with
 CC normal constraints on cell growth. A cell containing three recombinant
 CC DNA constructs was produced. These constructs encode an MDM2 protein
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
 CC to a transcriptional activation domain, and a reporter gene downstream
 CC from a DNA element which is recognised by the sequence-specific
 CC DNA-binding domain. The cell is used to identify a compound which
 CC interferes with the binding of MDM2 and p53. Since MDM2 is overexpressed
 CC in tumour cells and since binding of MDM2 to p53 appears to allow tumour
 CC cells to escape from p53-regulated growth, compounds that inhibit such
 CC binding would be useful as anti-cancer agents.
 XX SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 19; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 Db 1 GCACCGCGCAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 QY 61 GCAAGAACCGCAGCGGCGCGCGCGCGCCCTCTGACCGAGATCCTGCTGCTTTTCG 120
 Db 61 GCAAGAACCGCAGCGCGCGCGCGCGCCCTCTGACCGAGATCCTGCTGCTTTTCG 120
 QY 121 CAGCCAGGACACCTGCTCCCTCCCGGATTTAGTGTGCTAGAGGCGCCAGTGGCCCTGGCCCG 180
 Db 121 CAGCCAGGACACCTGCTCCCTCCCGGATTTAGTGTGCTAGAGGCGCCAGTGGCCCTGGCCCG 180
 QY 181 GAGAGTGAATGATCCCGCAGGCGCGCTGCTGCTTCCGCGAGTACAGTCCCGCTG 240
 Db 181 GAGAGTGAATGATCCCGCAGGCGCGCTGCTGCTTCCGCGAGTACAGTCCCGCTG 240
 QY 241 AAGGAACTGGGAGTCTTGGAGGACCCCGGACTCCAGCGGAAACCCCGGATGTGA 300
 Db 241 AAGGAACTGGGAGTCTTGGAGGACCCCGGACTCCAGCGGAAACCCCGGATGTGA 300
 QY 301 GGAGCAGGCAAAATGTGCAATATACCAATCTCTGTACTACTGATGCTGCTGTAAACCACT 360
 Db 301 GGAGCAGGCAAAATGTGCAATATACCAATCTCTGTACTACTGATGCTGCTGTAAACCACT 360
 QY 361 CACAGATTCAGCTTCGGAAACAGACACCTTATACTATGAAGAGGTTCTTTTATC 420
 Db 361 CACAGATTCAGCTTCGGAAACAGACACCTTATACTATGAAGAGGTTCTTTTATC 420
 QY 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATACTATGAAGAGGTTCTTTTATC 480
 Db 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATACTATGAAGAGGTTCTTTTATC 480
 QY 481 TTGGCCAGTATATATGACTAAACGATTATATGATGAGAGCAACACATATTTGATATT 540
 Db 481 TTGGCCAGTATATATGACTAAACGATTATATGATGAGAGCAACACATATTTGATATT 540

Qy	1621	CTGTGTGATTTGCTCAAGGTGCGACCTAAATAATGGTTGCATGTCTCATGGCAAAACAGAC	1680
Db	1621	CTTGTGTGATTTTGTCAAGGTGCGACCTAAATAATGGTTGCAATGTCTCATGGCAAAACAGAC	1680
Qy	1681	ATCTTATGGCTGCTTTACATGTGCAAGAAGCTTAAAGAAAGGAATTAAGCCCTGCCAG	1740
Db	1681	ATCTTATGGCTGCTTTACATGTGCAAGAAGCTTAAAGAAAGGAATTAAGCCCTGCCAG	1740
Qy	1741	TATGTAGACAACCAATTCAAATGATTTGCTTAACCTTAATTTCCCTTAGTTGACCTGTCTAT	1800
Db	1741	TATGTAGACAACCAATTCAAATGATTTGCTTAACCTTAATTTCCCTTAGTTGACCTGTCTAT	1800
Qy	1801	AAGAGAATTAATATTTCTTAACCTATATAACCTAGGAATTTAGACAACCTGAATTTTAT	1860
Db	1801	AAGAGAATTAATATTTCTTAACCTATATAACCTAGGAATTTAGACAACCTGAATTTAT	1860
Qy	1861	CACATATACAAAGTGAGAAAATGCCCTCAATTCACATAGATTTCTTCTTTAGTATTAAT	1920
Db	1861	CACATATATCAAAAGTGAGAAAATGCCCTCAATTCACATAGATTTCTTCTTTAGTATTAAT	1920
Qy	1921	TGACCTACTTTGGTGTAGTGGAAATAGTCAATTTACTATAATTTGACTTGAATATGTAGCT	1980
Db	1921	TGACCTACTTTGGTGTAGTGGAAATAGTCAATTTACTATAATTTGACTTGAATATGTAGCT	1980
Qy	1981	CATCCTTTACACCAACCTCCTTAATTTTAAATAATTTCTACTCTGTCTTAATGAGAAGTAC	2040
Db	1981	CATCCTTTACACCAACCTCCTTAATTTTAAATAATTTCTACTCTGTCTTAATGAGAAGTAC	2040
Qy	2041	TTGGTTTTTTTTTTCTTAAATATGTATATGACATTTAAATGTAACCTTATATATTTTTTTTG	2100
Db	2041	TTGGTTTTTTTTTTCTTAAATATGTATATGACATTTAAATGTAACCTTATATATTTTTTTTG	2100
Qy	2101	AGACCGAGCTCTGCTCTGTGTACCCAGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA	2160
Db	2101	AGACCGAGCTCTGCTCTGTGTACCCAGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA	2160
Qy	2161	AGCTCTGCCCTCCCGGGTTTCGCACCAATTTCTCTGCTCAGCTCCCAATTAGCTTGGCC	2220
Db	2161	AGCTCTGCCCTCCCGGGTTTCGCACCAATTTCTCTGCTCAGCTCCCAATTAGCTTGGCC	2220
Qy	2221	TACAGTCATCTGCCACACACCTTGGCTAAATTTTTTGTACTTTTAGTAGAGACAGGGTTTC	2280
Db	2221	TACAGTCATCTGCCACACACCTTGGCTAAATTTTTTGTACTTTTAGTAGAGACAGGGTTTC	2280
Qy	2281	ACCTGTGTAGCCAGATGTTCTCGATCTCCTGTACCTCTGATCCGCCACCTTCGCGCTCC	2340
Db	2281	ACCTGTGTAGCCAGATGTTCTCGATCTCCTGTACCTCTGATCCGCCACCTTCGCGCTCC	2340
Qy	2341	CAAAAGTGTGGGATTTACAGGCATGTAGCCACCG	2372
Db	2341	CAAAAGTGTGGGATTTACAGGCATGTAGCCACCG	2372

XX US5702903-A.
 XX 30-DEC-1997.
 XX 13-NOV-1995; 95US-0557393.
 XX 07-APR-1993; 93US-0044619.
 XX 07-APR-1992; 92US-0867840.
 XX 23-JUN-1992; 92US-0903103.
 XX 18-MAY-1994; 94US-0245500.
 XX (UJVO) UNIV JOHNS HOPKINS.
 XX Kinzler KW, Vogelstein B;
 XX WPI; 1998-076411/07.
 XX P-PSDB; AAW42971.
 XX Cell containing reporter construct containing human MDM2 and p53
 XX genes - for identifying compounds that interfere with binding of
 XX human MDM2 to human p53, useful as anti-cancer agents
 XX Disclosure; Coulms 21-26; 37pp; English.
 XX The present sequence encodes human MDM2. The MDM2 gene is amplified in
 XX some human tumours. The amplification of this gene is diagnostic of
 XX neoplasia or its potential. It is speculated that the MDM2 protein is a
 XX potential DNA binding protein that functions in the modulation of
 XX expression of other genes and, when present in excess, interferes with
 XX normal constraints on cell growth. A cell containing three recombinant
 XX DNA constructs was produced. These constructs encode an MDM2 protein
 XX fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
 XX to a transcriptional activation domain, and a reporter gene downstream
 XX from a DNA element which is recognised by the sequence-specific
 XX DNA-binding domain. The cell is used to identify a compound which
 XX interferes with the binding of MDM2 and p53. Since MDM2 is overexpressed
 XX in tumour cells and since binding of MDM2 to p53 appears to allow tumour
 XX cells to escape from p53-regulated growth, compounds that inhibit such
 XX binding would be useful as anti-cancer agents.
 XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
 XX
 XX Query Match 100.0%; Score 2372; DB 19; Length 2372;
 XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCACCGCGCAGCTGGCTGCTCTGGGGGCTGTGTGGCCCTGTGTGCGGAAGATGGA 60
 Db 1 GCACCGCGCAGCTGGCTGCTCTGGGGGCTGTGTGGCCCTGTGTGCGGAAGATGGA 60
 Qy 61 GCAAGAGCCGAGCCGAGGGGGGGCGGACCCCTCTGACCGAGATCTCTGCTGCTTTTCG 120
 Db 61 GCAAGAGCCGAGCCGAGGGGGGGCGGACCCCTCTGACCGAGATCTCTGCTGCTTTTCG 120
 Qy 121 CAGCCAGGACCGCTCCCTCCCGGATAGTGGGTACGAGCCGCGCCAGTCCCTGGCCCG 180
 Db 121 CAGCCAGGACCGCTCCCTCCCGGATAGTGGGTACGAGCCGCGCCAGTCCCTGGCCCG 180
 Qy 181 CAGAGTGGAGTATCCCGAGGCGGCGGCGCTGTGTCCCGAGTACGATCCCGCGTG 240
 Db 181 CAGAGTGGAGTATCCCGAGGCGGCGGCGCTGTGTCCCGAGTACGATCCCGCGTG 240
 Qy 241 AAGGAACTGGGGAGTCTTGAGGACCCCGGACTCCAGGCGGAAACCCCGGATGGTGA 300
 Db 241 AAGGAACTGGGGAGTCTTGAGGACCCCGGACTCCAGGCGGAAACCCCGGATGGTGA 300
 Qy 301 GGACGAGCAATCTGCAATACCAATCTGTGTACCTACTGTGTGCTGTAAACCACT 360
 Db 301 GGACGAGCAATCTGCAATACCAATCTGTGTACCTACTGTGTGCTGTAAACCACT 360
 Qy 361 CACAGATTCAGCTCGGAACAGAGACCCCTGGTTAGACCAAGCCATGCTTTTCAAGT 420
 Db 361 CACAGATTCAGCTCGGAACAGAGACCCCTGGTTAGACCAAGCCATGCTTTTCAAGT 420

Db 361 CACAGATTCAGCTCGGAACAGAGACCCCTGGTTAGACCAAGCCATGCTTTTCAAGT 420
 Qy 421 TATTAAGTCTGTTGGTGCACAAAAGACACTTATCTATGAAAGAGTCTTTTTTATC 480
 Db 421 TATTAAGTCTGTTGGTGCACAAAAGACACTTATCTATGAAAGAGTCTTTTTTATC 480
 Qy 481 TTGGCCAGTATATATGACTAAAGGATTATATGATGAGAAGCAACAACATATCTATAT 540
 Db 481 TTGGCCAGTATATATGACTAAAGGATTATATGATGAGAAGCAACAACATATCTATAT 540
 Qy 541 GTTCAATGATCTCTCTAGGAGATTGTTGGCGTGCACCAAGCTTCTGTGAAAGAGCACA 600
 Db 541 GTTCAATGATCTCTCTAGGAGATTGTTGGCGTGCACCAAGCTTCTGTGAAAGAGCACA 600
 Qy 601 GGAATAATATACCATGATCTACAGGAAGTGTAGTAGTCAATCAGCAGGAATCATCGG 660
 Db 601 GGAATAATATACCATGATCTACAGGAAGTGTAGTAGTCAATCAGCAGGAATCATCGG 660
 Qy 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTACCTTTGAAAGTGGAGTGATCAAAAGG 720
 Db 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTACCTTTGAAAGTGGAGTGATCAAAAGG 720
 Qy 721 ACCTGTACAGAGCTTCAGGAAGAGAACCTTCACTTCTACATTTGGTTCTTAGACCAT 780
 Db 721 ACCTGTACAGAGCTTCAGGAAGAGAACCTTCACTTCTACATTTGGTTCTTAGACCAT 780
 Qy 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
 Db 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
 Qy 841 GTGAAGCAACAAGAAAGCCACAAATCTGATGATATTTCCCTTTCTTTGATGAAAGCC 900
 Db 841 GTGAAGCAACAAGAAAGCCACAAATCTGATGATATTTCCCTTTCTTTGATGAAAGCC 900
 Qy 901 TGGCTCTCTGTATAGGGAGATATCTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 Db 901 TGGCTCTCTGTATAGGGAGATATCTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 Qy 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATTTGGTGG 1020
 Db 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATTTGGTGG 1020
 Qy 1021 ATCAGGATCAGTTTCAGATCAGTTAGTGTAGATTTGAAGTTGAATCTCTCCACATCAG 1080
 Db 1021 ATCAGGATCAGTTTCAGATCAGTTAGTGTAGATTTGAAGTTGAATCTCTCCACATCAG 1080
 Qy 1081 AAGATATAGCCCTTAGTGAAGAGGACAAAGTCTCAGATGAAGATGATGAGGTATATC 1140
 Db 1081 AAGATATAGCCCTTAGTGAAGAGGACAAAGTCTCAGATGAAGATGATGAGGTATATC 1140
 Qy 1141 AAGTACTGTGTATCAGGCGGGGAGTGTATACAGATTCAATTTGAAGAGATCCTGAAA 1200
 Db 1141 AAGTACTGTGTATCAGGCGGGGAGTGTATACAGATTCAATTTGAAGAGATCCTGAAA 1200
 Qy 1201 TTTCTCTAGCTGACATTTGGAAATGCACTTCAATGCAATGAATGAATCCCTCCCTTCCAT 1260
 Db 1201 TTTCTCTAGCTGACATTTGGAAATGCACTTCAATGCAATGAATGAATCCCTCCCTTCCAT 1260
 Qy 1261 CACATTCGAAACAGATGTTGGGCCCTTCCTGAGAAATGGCTTCTTGAAGATGAAGGAAAG 1320
 Db 1261 CACATTCGAAACAGATGTTGGGCCCTTCCTGAGAAATGGCTTCTTGAAGATGAAGGAAAG 1320
 Qy 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAACTCAACCAAGCTCAAGAGGGCT 1380
 Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAACTCAACCAAGCTCAAGAGGGCT 1380
 Qy 1381 TTGATGTTCTCTGATTTAAAAAACTATAGTGAATGATTTCCAGAGAGTCATGTTGAGG 1440
 Db 1381 TTGATGTTCTCTGATTTAAAAAACTATAGTGAATGATTTCCAGAGAGTCATGTTGAGG 1440
 Qy 1441 AAAATGATGATTAATTTACACAGCTTCCAAATCACAAGAAAGTGAAGACTATTTCTCAGC 1500
 Db 1441 AAAATGATGATTAATTTACACAGCTTCCAAATCACAAGAAAGTGAAGACTATTTCTCAGC 1500

QY 1501 CATCAACTTCTAGTAGCATTTATTTATAGCAGCCAAAGAGATGTGAAGAGTTTGAAGGG 1560
 DB 1501 CATCAACTTCTAGTAGCATTTATTTATAGCAGCCAAAGAGATGTGAAGAGTTTGAAGGG 1560
 QY 1561 AAGAAACCCCAAGCAAGAGAGTGTGGATCTAGTTTGGCCCTTAATCCCATTTGAC 1620
 DB 1561 AAGAAACCCCAAGCAAGAGAGTGTGGATCTAGTTTGGCCCTTAATCCCATTTGAC 1620
 QY 1621 CTTGTGTGATTTGTCAGTCTGACCTAAATATGTTGTCATTTGCCATGGCAAAACAGGAC 1680
 DB 1621 CTTGTGTGATTTGTCAGTCTGACCTAAATATGTTGTCATTTGCCATGGCAAAACAGGAC 1680
 QY 1681 ATCTTATGGCCCTTTACATGTGCAAGAGCTAAAGAAAGAGTAAGGCCCTGCCAG 1740
 DB 1681 ATCTTATGGCCCTTTACATGTGCAAGAGCTAAAGAAAGAGTAAGGCCCTGCCAG 1740
 QY 1741 TATGTAGCAACCAATTTCAATGATTTGCTAACTTATTTCCCTTACCTTACCTTGTCTAT 1800
 DB 1741 TATGTAGCAACCAATTTCAATGATTTGCTAACTTATTTCCCTTACCTTACCTTGTCTAT 1800
 QY 1801 AAGAGAAATATATTTCTTAACATATATACCTTAGGAATTTAGACAACCTGAAATTTAT 1860
 DB 1801 AAGAGAAATATATTTCTTAACATATATACCTTAGGAATTTAGACAACCTGAAATTTAT 1860
 QY 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
 DB 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
 QY 1921 TGACCTACTTTGTAGTGAATAGTAATACCTTACTATTAATTTGACTTGAATATGAGCT 1980
 DB 1921 TGACCTACTTTGTAGTGAATAGTAATACCTTACTATTAATTTGACTTGAATATGAGCT 1980
 QY 1981 CATCTTTACACCACTCTTAATTTAAATATTTCTACTCTGTCTTAAATGAGAGTAC 2040
 DB 1981 CATCTTTACACCACTCTTAATTTAAATATTTCTACTCTGTCTTAAATGAGAGTAC 2040
 QY 2041 TTGGTTTTTTTTTCTTAATATGATATGACATTTAAATGATATTAATTTATTTTATTT 2100
 DB 2041 TTGGTTTTTTTTTCTTAATATGATATGACATTTAAATGATATTAATTTATTTTATTT 2100
 QY 2101 AGACCGAGTCTTCTGTGTACCGAGCTGGAGTGCAGTGGTGTATCTTGGCTCACTGCA 2160
 DB 2101 AGACCGAGTCTTCTGTGTACCGAGCTGGAGTGCAGTGGTGTATCTTGGCTCACTGCA 2160
 QY 2161 AGCTTGCCTCCCGGGTTCGACCAATTTCTCTGCTCAGCTCCCAATTAAGCTTGCC 2220
 DB 2161 AGCTTGCCTCCCGGGTTCGACCAATTTCTCTGCTCAGCTCCCAATTAAGCTTGCC 2220
 QY 2221 TACAGTCACTGCGCACACACCTGGCTAATTTTGTACTTTTACTAGAGACAGGTTTC 2280
 DB 2221 TACAGTCACTGCGCACACACCTGGCTAATTTTGTACTTTTACTAGAGACAGGTTTC 2280
 QY 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCTGACCTCTGATCCGCCACCTTCGCCCTCC 2340
 DB 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCTGACCTCTGATCCGCCACCTTCGCCCTCC 2340
 QY 2341 CAAGTCTGGGATTACAGCATGAGCCACCG 2372
 DB 2341 CAAGTCTGGGATTACAGCATGAGCCACCG 2372

RESULT 10

ID AAZ37471
 AC AAZ37471 standard; cDNA; 2372 BP.

XX AAZ37471;

DT 07-JAN-2000 (first entry)

DE Human sarcoma p53-associated gene.

XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53;

KW cancer; antisense; modulation; oligonucleotide; expression;
 KW inhibition; hyperproliferation; blood cancer; brain cancer;
 KW breast cancer; lung cancer; soft tissue cancer; psoriasis; fibrosis;
 KW atherosclerosis; restenosis; ss.
 XX Homo sapiens.
 OS
 XX
 PN WO9949065-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 26-MAR-1999; 99WO-US06702.
 XX
 PR 26-MAR-1998; 98US-0048810.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;
 XX
 DR WPI; 1999-610754/52.
 XX
 PT New antisense compounds used to treat eg. hyperproliferative conditions
 PT
 PS Example 2; Page 79-81; 157pp; English.
 XX
 CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
 CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
 CC exemplification of the present invention. The present invention
 CC describes novel nucleotide antisense compounds, targeted to the 5'
 CC untranslated, translation termination codon, or 3' untranslated region
 CC of a nucleic acid encoding human mdm2, that modulates expression of
 CC human mdm2. The oligonucleotides mediate their effect by antisense
 CC inhibition of hyperproliferative gene expression. The antisense compound
 CC is used to treat an animal having a disease or condition associated
 CC with mdm2, particularly a hyperproliferative condition, more
 CC particularly cancer, especially of the blood, brain, breast, lung or soft
 CC tissue, or psoriasis, fibrosis, atherosclerosis or restenosis.
 XX
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 20; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCCGCGAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGAAGATGGA 60
 DB 1 GCACCCGCGAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGAAGATGGA 60
 QY 61 GCAAGAGCCGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 61 GCAAGAGCCGAGCG 120
 QY 121 CAGCCAGGAGCAGCGCTCCCTCCCGGATTTAGTGTGCGTACGAGCGCGCGCGCGCGCG 180
 DB 121 CAGCCAGGAGCAGCGCTCCCTCCCGGATTTAGTGTGCGTACGAGCGCGCGCGCGCG 180
 QY 181 GAGAGTGGATGATCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 DB 181 GAGAGTGGATGATCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 QY 241 AAGGAACTGGGAGTCTTTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 DB 241 AAGGAACTGGGAGTCTTTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 QY 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACTGTACTGTGTGTGTGTGTGTGTGT 360
 DB 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACTGTACTGTGTGTGTGTGTGTGTGT 360
 QY 361 CACAGATTTCCAGCTTCGGAAACAGAGACCGCTGTTAGACCAAGCAATTTGTTTGAAGT 420
 DB 361 CACAGATTTCCAGCTTCGGAAACAGAGACCGCTGTTAGACCAAGCAATTTGTTTGAAGT 420

QY 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATCTATGAAGAGGTTCTTTTTATC 480
 DB 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATCTATGAAGAGGTTCTTTTTATC 480
 QY 481 TTGGCCAGTATATATGACTAAACGATATATATGATGAGAACACACATATTTGATATT 540
 DB 481 TTGGCCAGTATATATGACTAAACGATATATATGATGAGAACACACATATTTGATATT 540
 QY 541 GTTCAATGATCTTCTAGCAGATTTGTTGGGTCGCCAAGCTTCTCTGTGAAGAGCACA 600
 DB 541 GTTCAATGATCTTCTAGCAGATTTGTTGGGTCGCCAAGCTTCTCTGTGAAGAGCACA 600
 QY 601 GGAATATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAAGAGGATCATCGG 660
 DB 601 GGAATATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAAGAGGATCATCGG 660
 QY 661 ACTCAGGTACATCTGAGTGAGACAGAGGTGTCACCTTGAAGGTGGAGTGATCAAAAGG 720
 DB 661 ACTCAGGTACATCTGAGTGAGACAGAGGTGTCACCTTGAAGGTGGAGTGATCAAAAGG 720
 QY 721 ACCTTGTACAAGAGCTTACAGGAAGAGAAACCTTTCATCTTCAATTTGGTTTCTAGACCAT 780
 DB 721 ACCTTGTACAAGAGCTTACAGGAAGAGAAACCTTTCATCTTCAATTTGGTTTCTAGACCAT 780
 QY 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGACAGAGAGAAATTCAGATGAATTTCTG 840
 DB 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGACAGAGAGAAATTCAGATGAATTTCTG 840
 QY 841 GTGAACGACAAAAGCCACAACTCTGATAGTATTTCCCTTTCTTTCATGAAGGCC 900
 DB 841 GTGAACGACAAAAGCCACAACTCTGATAGTATTTCCCTTTCTTTCATGAAGGCC 900
 QY 901 TGGCTCTGTGTAAAGGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 DB 901 TGGCTCTGTGTAAAGGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 QY 961 GGAGCCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATTTGGTGG 1020
 DB 961 GGAGCCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATTTGGTGG 1020
 QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAGAATTTGAAGTGAATCTCTGACTCAG 1080
 DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAGAATTTGAAGTGAATCTCTGACTCAG 1080
 QY 1081 AAGATTATACCTTTAGTGAAGAGGACAAAGACTCTCAGATCAAGATGATGAGGTATATC 1140
 DB 1081 AAGATTATACCTTTAGTGAAGAGGACAAAGACTCTCAGATCAAGATGATGAGGTATATC 1140
 QY 1141 AAGTTACTGTGTATCAGGCGAGGAGAGTGATACAGATTCATTTGAAGAAAGATCCTGAAA 1200
 DB 1141 AAGTTACTGTGTATCAGGCGAGGAGAGTGATACAGATTCATTTGAAGAAAGATCCTGAAA 1200
 QY 1201 TTTCCCTTAGCTGACTATTTGGAATGACATTCATGCAATGAATGAATCCCTCCCTTCCAT 1260
 DB 1201 TTTCCCTTAGCTGACTATTTGGAATGACATTCATGCAATGAATGAATCCCTCCCTTCCAT 1260
 QY 1261 CACATTCGAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCCCTGAAGATAAAGGGAAG 1320
 DB 1261 CACATTCGAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCCCTGAAGATAAAGGGAAG 1320
 QY 1321 ATAAGGGGAAATCTCTGAGAAAGCCAACTGGAATTCACACAAAGCTGAAGAGGCT 1380
 DB 1321 ATAAGGGGAAATCTCTGAGAAAGCCAACTGGAATTCACACAAAGCTGAAGAGGCT 1380
 QY 1381 TTGATGTTCTGATTTGAAAAAACHTATAGTGAATGATTTCCAGAGAGTCTGTTGAGG 1440
 DB 1381 TTGATGTTCTGATTTGAAAAAACHTATAGTGAATGATTTCCAGAGAGTCTGTTGAGG 1440
 QY 1441 AAAATGATGATAAAATTTACAAAGCTTCAATTCACAAAGAAAGTGAAGACTATTTCTCAGC 1500
 DB 1441 AAAATGATGATAAAATTTACAAAGCTTCAATTCACAAAGAAAGTGAAGACTATTTCTCAGC 1500
 QY 1501 CATCAACTTCTAGTAGCATTATTTATAGCAGCCAGAAAGATGTGAAGAGGTTGAAGGG 1560

DB 1501 CATCAACTTCTAGTAGCATTATTTATAGCAGCCAGAAAGATGTGAAGAGGTTGAAGGG 1560
 QY 1561 AAGAAACCCACAGACAAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
 DB 1561 AAGAAACCCACAGACAAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
 QY 1621 CTTGTGTGATTGTCAAGGTGCAGCTTAAATATGTTGCATTTGCATGGCAAAACAGGAC 1680
 DB 1621 CTTGTGTGATTGTCAAGGTGCAGCTTAAATATGTTGCATTTGCATGGCAAAACAGGAC 1680
 QY 1681 ATCTTATGGCTGCTTTACATGTGCAAGAAGCTTAAGAAAGAAAGAAATAGCCCTGCCAG 1740
 DB 1681 ATCTTATGGCTGCTTTACATGTGCAAGAAGCTTAAGAAAGAAAGAAATAGCCCTGCCAG 1740
 QY 1741 TATGTAGACAAACCAATTCAAATGATTGTCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
 DB 1741 TATGTAGACAAACCAATTCAAATGATTGTCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
 QY 1801 AAGAGAAATATATATTTCTAACTATATTAACCTTAGGAATTTAGACAACTGAAATTTATT 1860
 DB 1801 AAGAGAAATATATATTTCTAACTATATTAACCTTAGGAATTTAGACAACTGAAATTTATT 1860
 QY 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 DB 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 QY 1921 TGACCTTACTTTTGGTAGTGAATAGTACTTACTATTAATTTGACCTTGAATATGTAGCT 1980
 DB 1921 TGACCTTACTTTTGGTAGTGAATAGTACTTACTATTAATTTGACCTTGAATATGTAGCT 1980
 QY 1981 CATCTTTACACCAACTCCTTAATTTAAATATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 DB 1981 CATCTTTACACCAACTCCTTAATTTAAATATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 QY 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATTAATTAATTTATTTTGTG 2100
 DB 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATTAATTAATTTATTTTGTG 2100
 QY 2101 AGACCGAGTCTTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCAGTGA 2160
 DB 2101 AGACCGAGTCTTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCAGTGA 2160
 QY 2161 AGCTCTGCCCTCCCGGGTTCGCACCATTTCTCTGCCCTCAGCCTCCCAATTAGCTTGGCC 2220
 DB 2161 AGCTCTGCCCTCCCGGGTTCGCACCATTTCTCTGCCCTCAGCCTCCCAATTAGCTTGGCC 2220
 QY 2221 TACAGTCTCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGTAGACAGAGGTTTC 2280
 DB 2221 TACAGTCTCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGTAGACAGAGGTTTC 2280
 QY 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCCTGACCTGATCGCCACCTCGGCCCTCC 2340
 DB 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCCTGACCTGATCGCCACCTCGGCCCTCC 2340
 QY 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
 DB 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372

RESULT 11
 AAX35093
 -ID AAX35093 standard; cDNA; 2372 BP.
 XX
 AC AAX35093;
 XX
 DT 01-JUL-1999 (first entry)
 XX
 DE Nucleotide sequence of human MDM2 cDNA.
 XX
 KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
 inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
 XX

OS Homo sapiens.
XX W09910486-A2.
XX 04-MAR-1999.
XX 18-AUG-1998; 98WO-US17147.
XX 06-MAY-1998; 98US-0073567.
XX 22-AUG-1997; 97US-0916384.
XX (HYBR-) HYBRIDON INC.
XX Agrawal S, Chen J, Zhang R;
XX WPI; 1999-254219/21.
XX New MDM2-specific antisense oligonucleotides
XX Disclosure; Fig 1A; 59pp; English.
XX
XX The present sequence represents the cDNA sequence encoding human MDM2
XX protein. The specification describes antisense oligonucleotides that
XX inhibit MDM2 protein expression. The antisense oligonucleotides can
XX be used to activate a tumour suppressor. The antisense oligonucleotides
XX are used to inhibit tumour growth in a mammal, including a human,
XX particularly in conjunction with a DNA-damaging agent such as
XX camptothecin.
XX
XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
XX
XX Query Match 100.0%; Score 2372; DB 20; Length 2372;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GCACCGCGCAGCTTGGCTGCTTCTGGGCTGTGTGGCCCTGTGTGGCCCTGTGTGGAAAGATGGA 60
DB 1 GCACCGCGCAGCTTGGCTGCTTCTGGGCTGTGTGGCCCTGTGTGGCCCTGTGTGGAAAGATGGA 60
QY 61 GCAAGAAAGCCGAGCCGAGGGCGGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
DB 61 GCAAGAAAGCCGAGCCGAGGGCGGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
QY 121 CAGCCAGGACCGCTCCCTCCCGGATAGTGCCTAGCGAGCGCCAGTCCCTGCGCCG 180
DB 121 CAGCCAGGACCGCTCCCTCCCGGATAGTGCCTAGCGAGCGCCAGTCCCTGCGCCG 180
QY 181 GAGAGTGGAAATGATCCCGAGGCCCGAGGCGTCTGCTTCCGCACTAGTCACTCCCGTG 240
DB 181 GAGAGTGGAAATGATCCCGAGGCCCGAGGCGTCTGCTTCCGCACTAGTCACTCCCGTG 240
QY 241 AAGAAATCTGGGAGTCTTGGAGGACCCCGGACTCCAAAGCGGAAACCCCGGATGGA 300
DB 241 AAGAAATCTGGGAGTCTTGGAGGACCCCGGACTCCAAAGCGGAAACCCCGGATGGA 300
QY 301 GGACGAGCAATGTGCAATACCAATGCTGTACCTACTGATGGTGTCTTAACCACT 360
DB 301 GGACGAGCAATGTGCAATACCAATGCTGTACCTACTGATGGTGTCTTAACCACT 360
QY 361 CACAGATTCAGCTTCGGAACAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGT 420
QY 421 TATTAAAGTCTGTGGTGCACAAAGACACTTATACCTATGAAAGAGTCTTTTATC 480
DB 421 TATTAAAGTCTGTGGTGCACAAAGACACTTATACCTATGAAAGAGTCTTTTATC 480
QY 481 TTGCCAGTATATTAGCTAAACGATTATATGATGAGAAGCAACATATTGTATT 540
DB 481 TTGCCAGTATATTAGCTAAACGATTATATGATGAGAAGCAACATATTGTATT 540
QY 541 GTTCAATGATCTTAGGAGATTGTTGGCGTGCCAGCTTCTCTGTGAAGAGACA 600
DB 541 GTTCAATGATCTTAGGAGATTGTTGGCGTGCCAGCTTCTCTGTGAAGAGACA 600

DB 541 GTTCAATGATCTTAGGAGATTGTTGGCGTGCCAGCTTCTCTGTGAAGAGACA 600
QY 601 GGAAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
DB 601 GGAAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
QY 661 ACTCAGTACATCTGTGAGTGAAGAGTGTACCTTGAAGGTGGAGTGAAGTCAAGG 720
DB 661 ACTCAGTACATCTGTGAGTGAAGAGTGTACCTTGAAGGTGGAGTGAAGTCAAGG 720
QY 721 ACCTTGTACAGAGCTTTCAGGAAGAACCTTCACTCTCAGATTTGGTTCTAGACCAT 780
DB 721 ACCTTGTACAGAGCTTTCAGGAAGAACCTTCACTCTCAGATTTGGTTCTAGACCAT 780
QY 781 CTACCTCATCTAGAAGGAGCAATTTAGTGAGACAGAAAGAAATTCAGATGAATTTCTG 840
DB 781 CTACCTCATCTAGAAGGAGCAATTTAGTGAGACAGAAAGAAATTCAGATGAATTTCTG 840
QY 841 GTGAAGCAGAAAGAACCCACAAATCTGATGATTTTCCCTTTCTTTGATGAAGCC 900
DB 841 GTGAAGCAGAAAGAACCCACAAATCTGATGATTTTCCCTTTCTTTGATGAAGCC 900
QY 901 TGGCTCTGTGTGTAAGGAGATATTTGTGAAGAACGAGTACGAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTGTAAGGAGATATTTGTGAAGAACGAGTACGAGTGAATCTACAG 960
QY 961 GGAGCCATCGAATCCGGATCTTGATGCTGTGAAGTGAACATTCAGGTGATTTGGTGG 1020
DB 961 GGAGCCATCGAATCCGGATCTTGATGCTGTGAAGTGAACATTCAGGTGATTTGGTGG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAGTGAATTTGAAGTGAATCTCTCGACTCAG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAGTGAATTTGAAGTGAATCTCTCGACTCAG 1080
QY 1081 AAGATTATACCTTGTGAGGAGGAGTGTACAGATTTCAATGAAAGATGATGAGTATATC 1140
DB 1081 AAGATTATACCTTGTGAGGAGGAGTGTACAGATTTCAATGAAAGATGATGAGTATATC 1140
QY 1141 AAGTTACTGTGTATCAGGCGGAGAGTGTACAGATTTCAATGAAAGATGATGAGTATATC 1200
DB 1141 AAGTTACTGTGTATCAGGCGGAGAGTGTACAGATTTCAATGAAAGATGATGAGTATATC 1200
QY 1201 TTTCTTGTGTATCAGGCGGAGAGTGTACAGATTTCAATGAAAGATGATGAGTATATC 1260
DB 1201 TTTCTTGTGTATCAGGCGGAGAGTGTACAGATTTCAATGAAAGATGATGAGTATATC 1260
QY 1261 CACATTGCAACAGATTTGGGCGCTTCTGTGAGATTTGGCTTCTCTGAAGATGAAGGAAAG 1320
DB 1261 CACATTGCAACAGATTTGGGCGCTTCTGTGAGATTTGGCTTCTCTGAAGATGAAGGAAAG 1320
QY 1321 ATAAAGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAGCTGAAGAGGGCT 1380
DB 1321 ATAAAGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAGCTGAAGAGGGCT 1380
QY 1381 TTGATGTTCTGATTTAAAGAACTATAGTGAATTTGGCTTCTCTGAAGATGAAGGAAAG 1440
DB 1381 TTGATGTTCTGATTTAAAGAACTATAGTGAATTTGGCTTCTCTGAAGATGAAGGAAAG 1440
QY 1441 AAAATGATGATAAAATTTACAAAGCTTCAATCAAGAAAGTGAAGATTTCTCAGC 1500
DB 1441 AAAATGATGATAAAATTTACAAAGCTTCAATCAAGAAAGTGAAGATTTCTCAGC 1500
QY 1501 CATCACTTCTAGTACATTTATAGCGCCAGAGATTTGAAGTGAAGTGAAGG 1560
DB 1501 CATCACTTCTAGTACATTTATAGCGCCAGAGATTTGAAGTGAAGTGAAGG 1560
QY 1561 AAGAAACCCAGAACAAAGAGAGTGTGAATCTAGTTTCCCTTTAAATGCCATTGAAC 1620
DB 1561 AAGAAACCCAGAACAAAGAGAGTGTGAATCTAGTTTCCCTTTAAATGCCATTGAAC 1620
QY 1621 CTTCTGTGATTTCTCAGGTCGACCTTAAAGTGGTTCATTTGTCATGGGCAACAGGAC 1680
DB 1621 CTTCTGTGATTTCTCAGGTCGACCTTAAAGTGGTTCATTTGTCATGGGCAACAGGAC 1680

QY	1681	ATCTTATGGCCTGCTTTACATGTGCAAGAAGCTAAAGAAAAAGGAATAAGCCCTGGCCAG	1740
Db	1681	ATCTTATGGCCTGCTTTACATGTGCAAGAAGCTAAAGAAAAAGGAATAAGCCCTGGCCAG	1740
QY	1741	TATGTAGACAACCAATTCAATGATGTGTGACTTATTTCCCTAGTGTGACCTGTCTAT	1800
Db	1741	TATGTAGACAACCAATTCAATGATGTGTGCTACTTATTTCCCTAGTGTGACCTGTCTAT	1800
QY	1801	AAGAGAAATATATATTTCTPACTATATAACCCTAGGAATTTAGACAACCTGAAATTTATT	1860
Db	1801	AAGAGAAATATATATTTCTPACTATATAACCCTAGGAATTTAGACAACCTGAAATTTATT	1860
QY	1861	CACATATATCAAAAGTCAGAAAAATGCCCAATTCACATAGATTTCTTCCTTAGTATAAT	1920
Db	1861	CACATATATCAAAAGTCAGAAAAATGCCCAATTCACATAGATTTCTTCCTTAGTATAAT	1920
QY	1921	TGACCTACTTTGGTAGTGGAAATAGTGAATACTTACTATTAATTTGACTTGAATATGTAGCT	1980
Db	1921	TGACCTACTTTGGTAGTGGAAATAGTGAATACTTACTATTAATTTGACTTGAATATGTAGCT	1980
QY	1981	CATCCTTTTACACCAACTCCTAAATTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC	2040
Db	1981	CATCCTTTTACACCAACTCCTAAATTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC	2040
QY	2041	TGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTATTAATTTTTTTTG	2100
Db	2041	TGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTATTAATTTTTTTTG	2100
QY	2101	AGACCGAGTCTTGCTCTGTTACCCAGGCTGGAGTGAGTGGGTGATCTTGGCTCACTGCA	2160
Db	2101	AGACCGAGTCTTGCTCTGTTACCCAGGCTGGAGTGAGTGGGTGATCTTGGCTCACTGCA	2160
QY	2161	AGCTCTGCCCTCCCGGGTTCCACCAATTCCTGCGCTCAGCCCTCCCAATTAGCTTGGCC	2220
Db	2161	AGCTCTGCCCTCCCGGGTTCCGACCAATTCCTGCGCTCAGCCCTCCCAATTAGCTTGGCC	2220
QY	2221	TACAGTCATCTGCCACCAACCTGGCTCAATTTTTTGTACTTTTAGTAGAGACAGGGTTTC	2280
Db	2221	TACAGTCATCTGCCACCAACCTGGCTCAATTTTTTGTACTTTTAGTAGAGACAGGGTTTC	2280
QY	2281	ACCGTGTTAGCCAGGATGCTTCGATCCTCGATCCTGATCCGCCACCTCGGCCCTCC	2340
Db	2281	ACCGTGTTAGCCAGGATGCTTCGATCCTCGATCCTGATCCGCCACCTCGGCCCTCC	2340
QY	2341	CAAAGTCTGGGATTAACAGGCATGAGCAACG	2372
Db	2341	CAAAGTCTGGGATTAACAGGCATGAGCAACG	2372

RESULT 12
AAX03947
ID AAX03947 standard; cDNA; 2372 BP.

13-APR-1999 (first entry)

Human MDM2 encoding cDNA.

Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis; malignant fibrous histiocytoma; MFH; liposarcoma; ds.

XX Homo sapiens.
OS

XX	Key	Location/Qualifiers
FH	CDS	312..1787
FT		

XX
PN
US5858976-A.XX
12--TAN-1999
PD

XX

PF	14-FEB-1997;	97US-0801718.
XX		
PR	07-APR-1993;	93US-0044619.
PR	07-APR-1992;	92US-0867840.
PR	23-JUN-1992;	92US-0903103.
PR	17-FEB-1995;	95US-0390515.
PR	14-FEB-1997;	97US-0801718.
XX	(UYJO) UNIV JOHNS HOPKINS.	
XX	Burrell M, Hill DE, Kinzler KW, Vogelstein B;	
XX	WPI; 1999-152105/13.	
DR	P-PSDB; AAW94304.	
DR		
PPT	Inhibiting growth of tumour cells having MDM2 gene amplification -	
PPT	with MDM2-binding p53 fragment	
XX		
XX	Example 1; Column 19-24; 41pp; English.	
CC	The present invention describes: (1) a method for inhibiting the growth	
CC	of tumour cells which contain a human MDM2 gene amplification,	
CC	comprising administering to the cells a DNA molecule that expresses a	
CC	polypeptide consisting of a portion of p53 i.e. amino acids 13-41 of the	
CC	64 amino acid sequence given in AAW94303; the polypeptide being capable	
CC	of binding to human MDM2 (see AAW94304); (2) a method as in (1) where	
CC	the polypeptide lacks the homo-oligomerisation domain of p53; and (3) a	
CC	method as in (1) where the polypeptide lacks amino acids 138-393 of p53.	
CC	The method is useful for treating the following tumour types which have	
CC	a MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH),	
CC	M-20 MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, KL30	
CC	liposarcoma, and OSA-CL MFH. The present sequence encodes human MDM2.	
XX		
XX	Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;	
SQ		
	Query Match 100.0%; Score 2372; DB 20; Length 2372;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 GCACCGCGGAGCTTGGCTGTCTTCGGGGCCTGTGTGGCCCTGTGTGTCGGAAGATGGA 60	
Db	1 GCACCGCGGAGCTTGGCTGTCTTCGGGGCCTGTGTGGCCCTGTGTGTCGGAAGATGGA 60	
QY	61 GCAGAAGCCGAGCCCGAGGGGGCGGCACCCCTCTGACCGAGATCTGCTGTTTCG 120	
Db	61 GCAAGAAGCCGAGCCCGAGGGGGCGGCACCCTCTGACCGAGATCTGCTGTTTCG 120	
QY	121 CAGCCAGGAGCACCGTCCCTCCC CGGATTAGTGCTACGAGCGCCAGTGCCTGGCCCG 180	
Db	121 CAGCCAGGAGCACCGTCCCTCCC CGGATTAGTGCTACGAGCGCCAGTGCCTGGCCCG 180	
QY	181 GAGAGTGGAAATGATCCCCGAGGCCAGGGCGTGTGCTCCGCGAGTAGTCACTGCCCGTG 240	
Db	181 GAGAGTGGAAATGATCCCCGAGGCCAGGGCGTGTGCTCCGCGAGTAGTCACTGCCCGTG 240	
QY	241 AAGGAAACTGGGAGTCTTGAGGGACCCCGACTCCAAGCGCGAAAACCCCGATGGTGA 300	
Db	241 AAGGAAACTGGGAGTCTTGAGGGACCCCGACTCCAAGCGCGAAAACCCCGATGGTGA 300	
QY	301 GGAGCAGCAAATGTGCANATCAACAATGTCTGTACTACTGTGTGTGTGTGTGTGTGTGTGT 360	
Db	301 GGAGCAGCAAATGTGCANATCAACAATGTCTGTACTACTGTGTGTGTGTGTGTGTGTGTGT 360	
QY	361 CACAGATTCAGCTTCGGAACAGAGACCCCTGGTGTAGACAAAGCCATTTGCTTTTGAAGT 420	
Db	361 CACAGATTCAGCTTCGGRACAGAGACCCCTGGTGTAGACAAAGCCATTTGCTTTTGAAGT 420	
QY	421 TATTAAAGTCTGTGGTGCAAAAAGACACTTATTAATAAAGAGGTTCTTTTTTATC 480	
Db	421 TATTAAAGTCTGTGGTGCAAAAAGACACTTATTAATAAAGAGGTTCTTTTTTATC 480	
QY	481 TTGGCCAGTATATTATGACTTAACAGTATATGATGAGAAGCAACACATATTGTATATT 540	

Db 481 TTGCCAGTATATNTGACTAAACGNTTATATGATGAGAGCAACAACATATTGTATATT 540
 Qy 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGTGCCAGCTTCTCTGTGAAAGACACA 600
 Db 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGTGCCAGCTTCTCTGTGAAAGACACA 600
 Qy 601 GGAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
 Db 601 GGAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
 Qy 661 ACTCAGTACATCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGATCAAAAGG 720
 Db 661 ACTCAGTACATCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGATCAAAAGG 720
 Qy 721 ACCTTGTACAGAGCTTCTAGGAAGAGAAACCTTCTCATCTTCAATTTGCTTCTAGACCAT 780
 Db 721 ACCTTGTACAGAGCTTCTAGGAAGAGAAACCTTCTCATCTTCAATTTGCTTCTAGACCAT 780
 Qy 781 CTACCTCANTCAGAGGAGCAANTTACTGAGACAGAGAAATTCAGATGAATTTATCTG 840
 Db 781 CTACCTCANTCAGAGGAGCAANTTACTGAGACAGAGAAATTCAGATGAATTTATCTG 840
 Qy 841 GTGAACGACAAAGAAACCCACAACTCTGATAGTATTTCCCTTTCTTGTATCAAGCC 900
 Db 841 GTGAACGACAAAGAAACCCACAACTCTGATAGTATTTCCCTTTCTTGTATCAAGCC 900
 Qy 901 TGGCTCTGTGTGTAATAGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 Db 901 TGGCTCTGTGTGTAATAGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 Qy 961 GGAGCCATCGAATCCGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGTTGG 1020
 Db 961 GGAGCCATCGAATCCGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGTTGG 1020
 Qy 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAGATTTGAATGTCCTGACTCAG 1080
 Db 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAGATTTGAATGTCCTGACTCAG 1080
 Qy 1081 AAGATTATAGCTTGTAGGAAGACAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
 Db 1081 AAGATTATAGCTTGTAGGAAGACAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
 Qy 1141 AAGTTACTGTATCAGGCGGGAGAGTGATACAGATTTCAATTTGAAGAGATCCTGAA 1200
 Db 1141 AAGTTACTGTATCAGGCGGGAGAGTGATACAGATTTCAATTTGAAGAGATCCTGAA 1200
 Qy 1201 TTTCTTGTAGTACTATTTGGAATGCATTCATGCAATGAATCAATCCCGCTTCCAT 1260
 Db 1201 TTTCTTGTAGTACTATTTGGAATGCATTCATGCAATGAATCAATCCCGCTTCCAT 1260
 Qy 1261 CACATTGCAACAGATGTTGGGCCCTTCCGTGAGAAATTTGCTTCAAGATAAAGGGAAG 1320
 Db 1261 CACATTGCAACAGATGTTGGGCCCTTCCGTGAGAAATTTGCTTCAAGATAAAGGGAAG 1320
 Qy 1321 ATAAAGGGAAATCTCTGAGAAGCCAACTGGAAGAACTCAACAAAGCTGAAGAGGCT 1380
 Db 1321 ATAAAGGGAAATCTCTGAGAAGCCAACTGGAAGAACTCAACAAAGCTGAAGAGGCT 1380
 Qy 1381 TTGATGTTCTGATTTGTAATAAACTATAGTGAATGATTTCCAGAGAGTCTGTTGAGG 1440
 Db 1381 TTGATGTTCTGATTTGTAATAAACTATAGTGAATGATTTCCAGAGAGTCTGTTGAGG 1440
 Qy 1441 AAAATGATGATAAAATACAAAGCTTCAATCAACAAAGAAAGTGAAGACTATTTCTCAGC 1500
 Db 1441 AAAATGATGATAAAATACAAAGCTTCAATCAACAAAGAAAGTGAAGACTATTTCTCAGC 1500
 Qy 1501 CATCAACTTCTAGTACATTTATAGCAGCCAAAGAGATGTGAAGAGTTTGAAGGG 1560
 Db 1501 CATCAACTTCTAGTACATTTATAGCAGCCAAAGAGATGTGAAGAGTTTGAAGGG 1560
 Qy 1561 AAGAAACCCAAAGACAAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTGAAC 1620
 Db 1561 AAGAAACCCAAAGACAAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTGAAC 1620

Qy 1621 CTTGTGTGATTTGTCAAGTGCACCTAAAAATGGTTCGATTGGCCATGGCAAAACAGGAC 1680
 Db 1621 CTTGTGTGATTTGTCAAGTGCACCTAAAAATGGTTCGATTGGCCATGGCAAAACAGGAC 1680
 Qy 1681 ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAAGAAAAGGAATAAGCCCTGCCAG 1740
 Db 1681 ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAAGAAAAGGAATAAGCCCTGCCAG 1740
 Qy 1741 TATGTAGACAACCAATTCAAATGATGTCCTAACTATTTCCCTAGTTCACCTGTCTAT 1800
 Db 1741 TATGTAGACAACCAATTCAAATGATGTCCTAACTATTTCCCTAGTTCACCTGTCTAT 1800
 Qy 1801 AAGAGAATTATATTTCTTAACTATATAACCTTAGGAATTTAGACAACTTGAATTTAT 1860
 Db 1801 AAGAGAATTATATTTCTTAACTATATAACCTTAGGAATTTAGACAACTTGAATTTAT 1860
 Qy 1861 CACATATACAAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 Db 1861 CACATATACAAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 Qy 1921 TGACCTACTTTGGTAGTGAATAGTGAATCTTACTATAATTTGACTTGAATATGAGCT 1980
 Db 1921 TGACCTACTTTGGTAGTGAATAGTGAATCTTACTATAATTTGACTTGAATATGAGCT 1980
 Qy 1981 CATCCTTTACACCACTCTCTAAATTTAAATTAATTTCTCTCTCTTAAATGAGAAGTAC 2040
 Db 1981 CATCCTTTACACCACTCTCTAAATTTAAATTAATTTCTCTCTCTTAAATGAGAAGTAC 2040
 Qy 2041 TTGGTTTTTTTTTCTTAAATGATATGACATTTAAATGATTAATTTATTTTGTG 2100
 Db 2041 TTGGTTTTTTTTTCTTAAATGATATGACATTTAAATGATTAATTTATTTTGTG 2100
 Qy 2101 AGACCCAGCTTCTGTTTACCCAGGCTGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Db 2101 AGACCCAGCTTCTGTTTACCCAGGCTGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Qy 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTCCTCTGCTCAGCTCCCAATAGCTTGGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTCCTCTGCTCAGCTCCCAATAGCTTGGCC 2220
 Qy 2221 TACAGTCACTGCGCACACACCTGGCTAAATTTTGTACTTTTGTAGTACAGACAGGTTTC 2280
 Db 2221 TACAGTCACTGCGCACACACCTGGCTAAATTTTGTACTTTTGTAGTACAGACAGGTTTC 2280
 Qy 2281 ACCGTGTTAGCCAGGATGCTCTGATCTCTCAGCTCCGATCGCCACCTCGGCTCC 2340
 Db 2281 ACCGTGTTAGCCAGGATGCTCTGATCTCTCAGCTCCGATCGCCACCTCGGCTCC 2340
 Qy 2341 CAAAGTCTGGGATTTACAGGCATGAGCCACCG 2372
 Db 2341 CAAAGTCTGGGATTTACAGGCATGAGCCACCG 2372

RESULT 13

AAA29389
 ID AAA29389 standard; cDNA; 2372 BP.

XX AAA29389;

XX 12-SEP-2000 (first entry)

XX MDM2 oncoprotein coding sequence.

XX hst2; telomerase; catalytic subunit; reverse transcriptase; life-span;
 KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
 KW proliferation; immortal; tumour therapy; macular degeneration; activator;
 KW INK4; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 312..1787
 FT CDS


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/*tag= a
/product= MDM2_oncoprotein
```

WO2000031238-A2.

02-JUN-2000.

24-NOV-1999: 99WO-US27907

25-NOV-1998: 98US-0109891.

17-FEB-1999: 99US-0120549:

(GENE-) GENETICA INC.

Hannon GJ, Beach DH:

WPI: 2000-400055/34.

P-PSDB: AAY96567.

New method for increasing the proliferative capacity of cell lines comprises administering agents reversibly activating telomerase activity and reversibly inactivating Rb/INK4 and/or p53 pathways useful in treating age related diseases

Claim 5: page 119-120: 123pp: English.

This cDNA, designated hEST2, is a human telomerase catalytic subunit homologue of yeast EST2p and Euplotes plp23. hEST2 is a member of the reverse transcriptase family of enzymes.

The invention concerns methods and reagents for extending the life-span, e.g. the number of mitotic divisions, of a cell. The method relies on a activation of a telomerase activity and inhibition of one or both of a retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the division cycle. Binding of INK4 family members, e.g. the tumour suppressor p16INK4a, inhibits kinase activity and results in growth arrest. Rb inactivators can selectively and reversibly inactivate the Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MN2 is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor and can also be used in the methods. Other molecules which can be used include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which differs from at one or more of residues K22, R24, H95 and/or D97.

Additional constructs include a papilloma virus E7 protein, or other viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of the Rb and p16INK4a genes may also be used. The methods are useful for increasing the proliferative capacity of cells. The cells are subsequently of use in pharmaceutical and cosmetic preparations used to treat conditions related to (premature) aging, e.g. macular degeneration and arteriosclerosis. The cells can also be used to replace tumour cell lines in vitro and for studies on biochemical and physiological aspects of growth and differentiation. Long lived (immortal) cells could also be of use in the production of normal or genetically engineered biotechnology products.

Sequence 2372 BP: 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match	100.0%;	Score 2372;	DB 21;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2372:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGTCGGGAAGATGGA 60

61 GCAGAGCCGAGCCCGAGGGCGGGCCGAGATCCTGACCGAGATCCTGCTGCTTTCG 120

61 GCAGGACCCAGCCCAGGGCGGCCGCATCTGACCAGATCCTGATGCTTTTCG 120

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701 CACCEMCCAAECCACCACCACCACCACCACCACCACCACCACCACC

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Db 1321 ATAAGGGGAAATCTCTGAGAAAGCCAACTGGAAACTCAACAAAGCTGAAGAGGGCT 1380
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Db 1381 TTGATGTTCTGATTTGTAATAAACTATAGTGAATGATTCAGAGAGTCAATGTTGAGG 1440
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Db 1441 AAAATGATGATAAAATTCACAAAGCTTCACAAATCACAAGAAAGTGAAGACTATTCACG 1500
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Qy 1561 AAGAAACCCCAAGCAAGAGAGTGTGGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
Db 1561 AAGAAACCCCAAGCAAGAGAGTGTGGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
Qy 1621 CTTGTGTGATTTGTCAAGTGCACCTAAATATGTTGCTATGTCATGTCATGGCAAAACAGGAC 1680
Db 1621 CTTGTGTGATTTGTCAAGTGCACCTAAATATGTTGCTATGTCATGTCATGGCAAAACAGGAC 1680
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Db 1681 ATCTTATGGCTGCTTTACATCTGCAAGAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
Qy 1741 TATGTAGACCAACAAATTCAAATGATTTGCTGAATCTATTTCCCTAGTGAACCTGTCTAT 1800
Db 1741 TATGTAGACCAACAAATTCAAATGATTTGCTGAATCTATTTCCCTAGTGAACCTGTCTAT 1800
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Db 1801 AAGAGATATATATTTCTTAATCTATATAACCTAGGAATTTAGACAACCTGAAATTTAT 1860
Qy 1861 CACATATACAAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAT 1920
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Qy 1921 TGACCTACTTTGCTAGTGAATAGTGAATCTTACTATATTTGACTTGAATATGAGCT 1980
Db 1921 TGACCTACTTTGCTAGTGAATAGTGAATCTTACTATATTTGACTTGAATATGAGCT 1980
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Db 1981 CATCTTTACCAACTCTTAATTTAAATTAATTTCTACTCTGCTTAAATGAGAGTAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAATAATGATATGACATTTAAATGTAACCTTATTTATTTTGTG 2100
Db 2041 TTGGTTTTTTTTTTCTTAATAATGATATGACATTTAAATGTAACCTTATTTATTTTGTG 2100
Qy 2101 AGACCGAGTCTGCTCTGTTACCCAGGCTGGAGTGCAGTGGTGTCTTGGCTCACTGCA 2160
Db 2101 AGACCGAGTCTGCTCTGTTACCCAGGCTGGAGTGCAGTGGTGTCTTGGCTCACTGCA 2160
Qy 2161 AGCTCTGCCCTCCCGGTTGCGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Db 2161 AGCTCTGCCCTCCCGGTTGCGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Qy 2221 TACAGTCACTGCGCACACACCTGGCTAATTTTGTACTTTTGTAGTACAGAGGGTTTC 2280
Db 2221 TACAGTCACTGCGCACACACCTGGCTAATTTTGTACTTTTGTAGTACAGAGGGTTTC 2280
Qy 2281 ACCGTGTACGAGGATGCTCTGATCTCTGACCTCTGATCGCCGACCTGCGGCTCC 2340
Db 2281 ACCGTGTACGAGGATGCTCTGATCTCTGACCTCTGATCGCCGACCTGCGGCTCC 2340
Qy 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372

RESULT 14

AAS29240

ID AAS29240 standard; cDNA; 2372 BP.

XX AC AAS29240;

XX AT 21-NOV-2001 (first entry)

XX DE Human mdm2 cDNA sequence.

XX DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;

XX KW atherosclerosis; tumour; cytostatic; anti psoriatic;

XX KW anti arteriosclerotic; vasotropic; ss.

XX OS Homo sapiens.

XX PN US2001016575-A1.

XX PD 23-AUG-2001.

XX PF 02-JAN-2001; 2001US-0752983.

XX PR 26-MAR-1999; 99US-0280805.

XX PR 26-MAR-1998; 98US-0048810.

XX PA (MIRA/) MIRAGLIA L J.

XX PA (NERO/) NERO P.

XX PA (GRAH/) GRAHAM M J.

XX PA (MONI/) MONIA B P.

XX PA (COWS/) COWSERT L M.

XX PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;

XX DR WPI; 2001-535565/59.

XX PT An antisense compound, useful for treating e.g. cancer, comprises

XX PT nucleobases targeted a region (e.g. translation termination codon

XX PT region) of a nucleic acid encoding human mdm2 -

XX PS Example 2; Page 24-25; 81pp; English.

XX CC The present invention relates to antisense compounds (AAS29242-AAS29507),

XX CC 8-30 nucleobases in length targeted to the 5' untranslated region,

XX CC translation termination codon region, 3' untranslated region, coding

XX CC region or translation start site of a nucleic acid encoding human mdm2,

XX CC where the antisense compound modulates the expression of human mdm2.

XX CC The antisense oligonucleotides of the invention are useful for encoding

XX CC human mdm2 and for inhibiting the expression of human mdm2. They may be

XX CC used for treating an animal having a disease or condition associated

XX CC with amplification of mdm2 gene or overexpression of mdm2 e.g. a

XX CC hyperproliferative disorder such as cancer (blood, brain, breast, lung,

XX CC or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or

XX CC restenosis, tumours, colorectal carcinoma and chronic myelogenous

XX CC leukemia. The antisense compound may be administered with a

XX CC chemotherapeutic agent to overcome drug resistance. The antisense

XX CC compound reduces hyperproliferation of human cells. The method, which

XX CC involves the use of the antisense compound, is also useful for detecting

XX CC the role of mdm2 expression in various cell functions and physiological

XX CC processes and useful in both clinical research and diagnostic tools.

XX CC The present cDNA sequence encodes for human mdm2.

XX SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 22; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCGGAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGAAAGATGGA 60

Db 1 GCACCGCGGAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGAAAGATGGA 60

Db 2221 TACAGTCATCTGCACACACTGGCTAAATTTTGTACTTTTAGTAGACAGGTTTC 2280
Qy 2281 ACCGTTTACGAGATGGTCTGATCTCCCTGACCTCGTATCGGCCACCTCGGCTCC 2340
Db 2281 ACCGTTTACGAGATGGTCTGATCTCCCTGACCTCGTATCGGCCACCTCGGCTCC 2340
Qy 2341 CAAAGTCTGGGATTACAGCATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTACAGCATGAGCCACCG 2372

RESULT 15
AAD07530
ID AAD07530 standard; DNA; 2372 BP.
XX
AC AAD07530;
DT 10-AUG-2001 (first entry)
XX
DE Human p-53 associated mdm2 gene.
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; ds.
XX
OS Homo sapiens.
XX
PN US6238921-B1.
XX
PD 29-MAY-2001.
XX
PF 26-MAR-1998; 9805-0048810.
XX
PR 26-MAR-1998; 9805-0048810.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero P, Graham MJ, Monia BP;
XX
DR WPI; 2001-366477/38.
XX
PT New oligonucleotides 16506, 16507, 16518, 16520, 16521, 16522 and
PT 16524, which inhibits human mdm2 expression, useful for inhibiting,
PT diagnosing or treating abnormal proliferative conditions associated
PT with mdm2 -
XX
PS Example 2; Column 19-24; 19pp; English.
XX
CC The present invention relates to compositions and methods for modulating
CC the expression of human mdm2 gene, a naturally present cellular gene
CC implicated in abnormal cell proliferation and tumour formation. The
CC invention also provides antisense oligonucleotides which are targeted
CC to the mdm2 gene and are capable of inhibiting the expression of mdm2
CC gene. The oligonucleotides are useful in diagnostics, therapeutics,
CC prophylaxis and as research reagents. They are especially useful for
CC inhibiting, diagnosing and treating abnormal proliferative conditions
CC associated with mdm2. The method is useful for detecting and determining
CC the role of mdm2 expression in various cell functions and physiological
CC processes and conditions, and for diagnosing conditions associated with
CC mdm2 expression. The present sequence is p-53 associated mdm2 gene from
CC human.
XX
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 22; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCGGAGCTTGGCTGCTTCGCGGCTGTGTGSCCTGTGTGCGGAAGATGGA 60
Db 1 GCACCGCGGAGCTTGGCTGCTTCGCGGCTGTGTGSCCTGTGTGCGGAAGATGGA 60

Qy 61 GCAGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 1141 AGTTTACTGTGTATAGGCGGCGGAGGTGATACAGATTTCATTTTGAAGAGATCCTGAA 1200

Db 61 GCAGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Qy 121 CAGCCAGAGAGACCGTCCCTCCCGGATTAAGTGGTACGAGCGGCCAGTGCCCTGCCCG 180
Db 121 CAGCCAGAGAGACCGTCCCTCCCGGATTAAGTGGTACGAGCGGCCAGTGCCCTGCCCG 180
Qy 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTCGTGTCCGAGTAGTCAGTCCCGCGTG 240
Db 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTCGTGTCCGAGTAGTCAGTCCCGCGTG 240
Qy 241 AAGGAAACTGGGAGTCTTGAGGACCCCGGACCTCCAAAGCGGAAACCCCGATGGTGA 300
Db 241 AAGGAAACTGGGAGTCTTGAGGACCCCGGACCTCCAAAGCGGAAACCCCGATGGTGA 300
Qy 301 GGAGCAGGCAAAATGTGCAATACCAACATGTGTACCTACTGTGTGTGTGTGTGTGTGT 360
Db 301 GGAGCAGGCAAAATGTGCAATACCAACATGTGTACCTACTGTGTGTGTGTGTGTGTGT 360
Qy 361 CACAGATTCAGCTTCGGGAACAGAGACCCCTGCTTACCCAAAGCCCATTTGCTTTGAAGT 420
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Qy 421 TATTTAAAGTCTGTGTGTGCACAAAAGACACTTATCTATGTAAGAGAGTCTTTTATC 480
Db 421 TATTTAAAGTCTGTGTGTGCACAAAAGACACTTATCTATGTAAGAGAGTCTTTTATC 480
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Qy 601 GGAAATATATACCATGATCTACAGAACTTGTGTAGTAGTCAATCAGCAGGAATCATCG 660
Db 601 GGAAATATATACCATGATCTACAGAACTTGTGTAGTAGTCAATCAGCAGGAATCATCG 660
Qy 661 ACTCAGGTACATCTGTGAGTGAGAACAGCTGTACCTTGAAGTGGGAGTGATCAAAAG 720
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Qy 721 ACCTTGTACAAGAGCTTTCAGGAAGAGAACTTCTATCTTACATTTGTTTCTAGACCAT 780
Db 721 ACCTTGTACAAGAGCTTTCAGGAAGAGAACTTCTATCTTACATTTGTTTCTAGACCAT 780
Qy 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGAGAAATTCAGATGAATTTATCTG 840
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Qy 841 GTGAAGCAGAAAGAAACCCCAAAATCTGATAGTATTTCCCTTTCTTTGATGAAAGCC 900
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Db 1021 ATCAGATTCAGTTTCAGATCAGTTTACTGTAGTATTTGAAGTGAATCTCTGAGCTCAG 1080
Qy 1081 AAGATTATACCTTTAGTGAAGAGACCAAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
Db 1081 AAGATTATACCTTTAGTGAAGAGACCAAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
Qy 1141 AAGTTACTGTGTATCAGGCGGAGAGGTGATACAGATTTCATTTTGAAGAGATCCTGAA 1200
Db 1141 AAGTTACTGTGTATAGGCGGAGAGGTGATACAGATTTCATTTTGAAGAGATCCTGAA 1200

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QY 1201 TTTCCTTAGCTGACTATTGGAAATGCACTTCATGCAATGAAATGCAATCCCGCTCCAT 1260
Db 1201 TTTCCTTAGCTGACTATTGGAAATGCACTTCATGCAATGAAATGCAATCCCGCTCCAT 1260
QY 1261 CACATTTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCTGAGATTAAGGGAAG 1320
Db 1261 CACATTTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCTGAGATTAAGGGAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAACTCAACACAGCTGAAGGGCT 1380
Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAACTCAACACAGCTGAAGGGCT 1380
QY 1381 TTGATGTTCTGATGTTAAATAAATACTATAGTGAATTTCCAGAGAGTCTATGTTGAGG 1440
Db 1381 TTGATGTTCTGATGTTAAATAAATACTATAGTGAATTTCCAGAGAGTCTATGTTGAGG 1440
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Db 1801 AAGAGAATTTATATTTCTAACTATATAACCTTAGGAATTTAGACAACTGAAATTTAT 1860
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QY 2101 AGACCGAGTCTGCTCTTACCCAGCTGGAGTGCAGTGGGTCATCTTGGCTCACTGCA 2160
Db 2101 AGACCGAGTCTGCTCTTACCCAGCTGGAGTGCAGTGGGTCATCTTGGCTCACTGCA 2160
QY 2161 AGCTCTGCCCTCCCGGGTTCGCCACCAATCTCTGCTCAGCTCCCAATAGCTTGGCC 2220
Db 2161 AGCTCTGCCCTCCCGGGTTCGCCACCAATCTCTGCTCAGCTCCCAATAGCTTGGCC 2220
QY 2221 TACAGTCACTGCCACCACTGCTGCTAATTTTGTACTTTTGTAGTACAGAGGTTTC 2280
Db 2221 TACAGTCACTGCCACCACTGCTGCTAATTTTGTACTTTTGTAGTACAGAGGTTTC 2280

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Db 2281 ACCGTGTTAGCCAGGATGGTCTCGATCTCTTGACCTCGTATCCGCCACCTCGGCTCC 2340
QY 2341 CAAAGTGTGGGATTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTACAGGATGAGCCACCG 2372

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Job time : 494 secs

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2003, 10:52:24 : Search time 87 Seconds
(without alignments)
8361.348 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2372	100.0	2372	1 US-07-903-103-1	Sequence 1, Appl
2	2372	100.0	2372	1 US-08-044-619A-1	Sequence 1, Appl
3	2372	100.0	2372	1 US-08-283-911-1	Sequence 1, Appl
4	2372	100.0	2372	1 US-08-245-500A-2	Sequence 2, Appl
5	2372	100.0	2372	1 US-08-390-546-2	Sequence 2, Appl
6	2372	100.0	2372	1 US-08-390-479A-2	Sequence 2, Appl
7	2372	100.0	2372	1 US-08-557-393-2	Sequence 2, Appl
8	2372	100.0	2372	1 US-08-390-516C-2	Sequence 2, Appl
9	2372	100.0	2372	1 US-08-390-517A-2	Sequence 2, Appl
10	2372	100.0	2372	1 US-08-390-515A-2	Sequence 2, Appl
11	2372	100.0	2372	2 US-08-801-718-2	Sequence 1, Appl
12	2372	100.0	2372	3 US-09-073-567-1	Sequence 1, Appl
13	2372	100.0	2372	4 US-09-280-805-1	Sequence 1, Appl
14	2372	100.0	2372	4 US-09-048-810-1	Sequence 1, Appl
15	2372	100.0	2372	4 US-09-170-159A-2	Sequence 2, Appl
16	2372	100.0	2372	4 US-09-480-718-43	Sequence 43, Appl
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18	975.6	41.1	1710	1 US-08-044-619A-3	Sequence 3, Appl
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20	975.6	41.1	1710	1 US-08-245-500A-4	Sequence 4, Appl
21	975.6	41.1	1710	1 US-08-390-546-4	Sequence 4, Appl
22	975.6	41.1	1710	1 US-08-390-479A-4	Sequence 4, Appl
23	975.6	41.1	1710	1 US-08-557-393-4	Sequence 4, Appl
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31	812.4	34.2	891	4 US-09-167-322-5	Sequence 5, Appl
32	812.2	34.2	966	4 US-09-167-322-7	Sequence 7, Appl
33	652	27.5	652	4 US-09-510-252-3	Sequence 3, Appl
34	576	24.3	657	4 US-09-167-322-6	Sequence 6, Appl
35	313	13.2	399	4 US-09-167-322-8	Sequence 8, Appl
36	227.2	9.6	309	4 US-09-167-322-9	Sequence 9, Appl
37	223	9.4	3609	4 US-09-705-399-11	Sequence 11, Appl
38	219.6	9.3	246240	2 US-08-724-394A-20	Sequence 20, Appl
39	219.6	9.3	246240	2 US-08-724-394A-21	Sequence 21, Appl
40	219.6	9.3	246240	1 US-08-724-394A-22	Sequence 22, Appl
41	218.8	9.2	3742	1 US-08-694-915-5	Sequence 5, Appl
42	217.2	9.2	320	1 US-08-629-939-5	Sequence 5, Appl
43	217.2	9.2	320	1 US-08-759-873-5	Sequence 5, Appl
44	217.2	9.2	38564	4 US-09-734-673-3	Sequence 3, Appl
45	216	9.1	87543	4 US-09-791-211-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-07-903-103-1
; Sequence 1, Application US/07903103
; Patent No. 5411860
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDW2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; APPLICATION NUMBER: US/07/903,103
; FILING DATE: 19920623
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867.840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: CaCo-2
; POSITION IN GENOME:

; MAP POSITION: 12q12-14

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 312..1784

US-07-903-103-1

Query Match 100.0%; Score 2372; DB 1; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCGCAGCTTGGCTCTTCTGGGCCCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60

Db 1 GCACCGCGCAGCTTGGCTCTTCTGGGCCCTGTGTGGGCCCTGTGTGCGGAAAGATGGA 60

Qy 61 GCAGAGCCGAGCCGAGGGGGGGGACCCCTCTGACCGAGATCCTGCTGCTTCG 120

Db 61 GCAGAGCCGAGCCGAGGGGGGGGACCCCTCTGACCGAGATCCTGCTGCTTCG 120

Qy 121 CAGCCAGGAGCAGCGTCCCTCCCGGATTAGTGCCTACGAGGCCAGTGCCCTGGGCCG 180

Db 121 CAGCCAGGAGCAGCGTCCCTCCCGGATTAGTGCCTACGAGGCCAGTGCCCTGGGCCG 180

Qy 181 GAGAGTGGATGATCCCGAGGCCAGGGCTGCTGCTCCGCACTAGTCACTGCCGCTG 240

Db 181 GAGAGTGGATGATCCCGAGGCCAGGGCTGCTGCTCCGCACTAGTCACTGCCGCTG 240

Qy 241 AAGGAAACTGGGAGTCTTGAGGGACCCCGACTCCAGCGCGAAACCCCGGATGTGA 300

Db 241 AAGGAAACTGGGAGTCTTGAGGGACCCCGACTCCAGCGCGAAACCCCGGATGTGA 300

Qy 301 GGACGAGCAATGTGCAATACCAAGATGCTGTACCTACTGATGGTCTGTACCCACT 360

Db 301 GGACGAGCAATGTGCAATACCAAGATGCTGTACCTACTGATGGTCTGTACCCACT 360

Qy 361 CACAGATCCAGCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTTGTAAGT 420

Db 361 CACAGATCCAGCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTTGTAAGT 420

Qy 421 TATTAAAGTCTGGTGCACAAAGAGACTTATCTATGATGAAGAGTCTTTTATC 480

Db 421 TATTAAAGTCTGGTGCACAAAGAGACTTATCTATGATGAAGAGTCTTTTATC 480

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Db 721 ACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCAATTTGGTTCTAGACCAT 780

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Db 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATTAATCTG 840

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Db 841 GTGAACGACAAAGAAACGCCCAAACTCTGATAGTATTTCCCTTTTGTGATAAGGCC 900

Qy 901 TGGCTCTGTGTATTAAGGGAGATATGTTGTAAGAGAGCAGTAGCAGTGAATCTACAG 960

Db 901 TGGCTCTGTGTATTAAGGGAGATATGTTGTAAGAGAGCAGTAGCAGTGAATCTACAG 960

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Db 1141 AAGTTTACTGTGTATCAGCGAGGAGAGTATACAGATTCATTTGAAGAGATCCCTGAAA 1200

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Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACACAGCTGAAGAGGGCT 1380

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Db 1381 TTGATGTTCTTGATGTATATAAAACTATAGTAATGATTCACAGAGATCATGTGTTGAGG 1440

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Db 1441 AAAATGATGATAAAATTACACAAGCTTCAACAATCACAAGAAAGTGAAGACTATCTCAGC 1500

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Db 1501 CATCAACTCTAGTAGCATTTATATAGCAGCCAGAAAGATGTGAAGAGTTTGAAGGG 1560

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Db 1561 AAGAAACCCAAAGACAAGAGAGTGTGGAATCTAGTTTGCCCTTTAATGCAATTTGAAC 1620

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Db 1621 CTTGTGCTATTGTCAAGGTGCACTTAAATGGTTGCATTTGCCATGCAACACAGNC 1680

Qy 1681 ATCTTATGGCCTGCTTTACATGTGCAAGAGCTAAAGAAAGAAATAAGCCCTGCCAG 1740

Db 1681 ATCTTATGGCCTGCTTTACATGTGCAAGAGCTAAAGAAAGAAATAAGCCCTGCCAG 1740

Qy 1741 TATGTAGACAACCAATTCAAATGATGTGCTAACTTATTTCCCTTAGTTGACCTGCTAT 1800

Db 1741 TATGTAGACAACCAATTCAAATGATGTGCTAACTTATTTCCCTTAGTTGACCTGCTAT 1800

Qy 1801 AAGAGAAATATATATTTCTAACTATTAACCCCTAGGAATTTAGACAACCTGAAATTTAT 1860

Db 1801 AAGAGAAATATATATTTCTAACTATTAACCCCTAGGAATTTAGACAACCTGAAATTTAT 1860

Qy 1861 CACATATATCAAGTGAGAAATGCCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920

Db 1861 CACATATATCAAGTGAGAAATGCCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920

Qy 1921 TGACCTACTTTGGTAGTGAATAGTAACTTACTATATAATTTGACTTCAATATGTAGCT 1980

Db 1921 TGACCTACTTTGGTAGTGAATAGTAACTTACTATATAATTTGACTTCAATATGTAGCT 1980

Qy 1981 CATCTCTTACACCAACCTCCTTAATTTTAAATTTTCTACTCTCTTAAATGAGAGTAC 2040

Db 1981 CATCTCTTACACCAACCTCCTTAATTTTAAATTTTCTACTCTCTTAAATGAGAGTAC 2040

Qy	2041	TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACTTATATTTTTTTG	2100
Db	2041	TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACTTATATTTTTTTG	2100
Qy	2101	AGACCGAGCTCTTGCTCTGTTTACCACAGGCTGGAGTGCAGTGGGTGATCTTTGGCTCACTGCA	2160
Db	2101	AGACCGAGCTCTGCTCTGTTTACCACAGGCTGGGTGAGTCTTTGGCTCACTGCA	2160
Qy	2161	AGCTCTGCCCTCCCGGGTTTCGACACATTCCTTCGCTCAGCCTCCCAATTAGCTTGGCC	2220
Db	2161	AGCTCTGCCCTCCCGGGTTTCGACACATTCCTTCGCTCAGCCTCCCAATTAGCTTGGCC	2220
Qy	2221	TACAGTCATCTGCCACACACACCTTGGCTAAATTTTTTTTACTTTTGTAGAGACAGAGGTTTC	2280
Db	2221	TACAGTCATCTGCCACACACACCTTGGCTAAATTTTTTTTACTTTTGTAGAGACAGAGGTTTC	2280
Qy	2281	ACCGTGTGTAGCCAGGATGCTCTGATCTCTGACCTCGTGTATCCGCCACCTCGGCCCTCC	2340
Db	2281	ACCGTGTGTAGCCAGGATGCTCTGATCTCTGACCTCGTGTATCCGCCACCTCGGCCCTCC	2340
Qy	2341	CAAAAGTCTGGGATTACAGGCATGAGCCACCG	2372
Db	2341	CAAAAGTCTGGGATTACAGGCATGAGCCACCG	2372

RESULT 2

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US-08-044-619A-1
; Sequence 1, Application US/08044619A
; Patent No. 5420263
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,619A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMBB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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QY	901	TG	CT	CT	GT	GT	TA	TA	AA	GG	G	A	G	A	T	A	T	T	G	T	G	A	A	A	G	A	G	C	A	G	T	A	G	A	A	T	C	T	A	C	A	G	960						
DB	901	TG	CT	CT	GT	GT	TA	TA	AA	GG	G	A	G	A	T	A	T	T	G	T	G	A	A	A	G	A	G	C	A	G	T	A	G	A	A	T	C	T	A	C	A	G	960						
QY	961	GG	AC	GC	AT	CG	GA	TC	CG	GA	T	CT	GT	G	T	G	T	AA	GT	GA	A	C	T	T	C	A	GT	T	C	A	GT	T	C	A	GT	T	C	A	GT	T	C	A	G	1020					
DB	961	GG	AC	GC	AT	CG	GA	T	CT	GT	G	T	G	T	AA	GT	GA	A	C	T	T	C	A	GT	T	C	A	GT	T	C	A	GT	T	C	A	GT	T	C	A	GT	T	C	A	G	1020				
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DB	1021	AT	C	A	G	A	T	T	C	A	G	A	T	C	A	G	A	T	T	C	A	G	A	T	T	C	A	G	A	T	T	C	A	G	A	T	T	C	A	G	A	T	C	A	G	1080			
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QY	1141	AA	G	T	T	A	C	T	G	T	A	C	A	G	C	A	G	G	G	A	G	A	G	T	G	A	T	T	C	A	T	T	C	A	T	T	T	G	A	A	G	A	T	C	T	G	A	A	1200
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QY	1381	T	T	C	A	T	G	T	T	C	A	T	T																																				

Qy	1981	CATCCTTTACACCAACTCTCTAAATTTTAAATATATTTCTACTCTCTGTCTTAATAGAGAAGTAC	2041	TTGGTGTCTTTTCTTTAAATATGTATATGACATTTAAATGTAACTTATATATTTTTTTTG	2100
Db	1981	CATCCTTTTACACCAACTCTCTAAATTTTAAATATATTTCTACTCTCTGTCTTAATAGAGAAGTAC	2040	TTGGTGTCTTTTCTTTAAATATGTATATGACATTTAAATGTAACTTATATATTTTTTTTG	2100
Qy	2041	TTGGTGTCTTTTCTTTAAATATGTATATGACATTTAAATGTAACTTATATATTTTTTTTG	2100	TTGGTGTCTTTTCTTTAAATATGTATATGACATTTAAATGTAACTTATATATTTTTTTTG	2100
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Db	2101	AGACCGAGTCTTGCTCTGTTTACCAGGCTGGAGTGCAGTGGGTGATCTTTGGCTCACTGCA	2160	AGCTCTGCGCCCTCCCGGGTTCGCACCATTTCTCTGCTCAGCCTCCCAATTAAGCTTTGGCC	2220
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Db	2161	AGCTCTGCGCCCTCCCGGGTTCGCACCATTTCTCTGCTCAGCCTCCCAATTAAGCTTTGGCC	2220	AGCTCTGCGCCCTCCCGGGTTCGCACCATTTCTCTGCTCAGCCTCCCAATTAAGCTTTGGCC	2220
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Db	2221	TACAGTCATCTGCCACACACACACCTGGCTAAATTTTGTACTTTTAGTAGAGACAGAGTTTC	2280	TACAGTCATCTGCCACACACACACCTGGCTAAATTTTGTACTTTTAGTAGAGACAGAGTTTC	2280
Qy	2281	ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCCTCC	2340	ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCCTCC	2340
Db	2281	ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCCTCC	2340	ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCCTCC	2340
Qy	2341	CXAAAGTCTGGGATACAGGCATGAGCCACCG	2372	CXAAAGTCTGGGATACAGGCATGAGCCACCG	2372
Db	2341	CXAAAGTCTGGGATACAGGCATGAGCCACCG	2372	CXAAAGTCTGGGATACAGGCATGAGCCACCG	2372

RESULT 3

US-08-283-911-1

; Sequence 1, Application US/08283911

; Patent No. 5519118

; GENERAL INFORMATION:

; APPLICANT: VOGELSTEIN, BERT

; APPLICANT: KINZLER, KENNETH

; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

; TITLE OF INVENTION: HUMAN TUMORS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

; STREET: 1001 G ST., N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20001-4597

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/283,911

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/903,103

; FILING DATE: 23-JUN-1992

; APPLICATION NUMBER: US 07/867,840

; FILING DATE: 07-APR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: KAGAN, SARAH A.

; REGISTRATION NUMBER: 32,141

; REFERENCE/DOCKET NUMBER: 01107.40148

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-508-9100

; TELEFAX: 202-508-9299

; TELEX: 197430 BMB UT

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2372 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: CaCo-2
; POSITION IN GENOME:
; MAP POSITION: 12q12-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
; US-08-283-911-1

Query Match      100.0%; Score 2372; DB 1: Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCACCGCGAGCTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGGAAGATGCA 60

QY 61 GCAAGAACGCGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 61 GCAAGAACGCGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

QY 121 CAGCAGGAGCAGCTCCCTCCCGGATTAGTGGTACGAGCGCGCGCGCGCGCGCG 180
DB 121 CAGCAGGAGCAGCTCCCTCCCGGATTAGTGGTACGAGCGCGCGCGCGCGCG 180

QY 181 GAGAGTGGAAATGATCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
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DB 301 GGAGAGGCAATGTGCAATACCAATGCTGTACCTACTGTATGATGATGATGATG 360

QY 361 CACAGATTCAGCTTCGGAACAGAGACCTGGTTAGACCAAGCCATTCCTTTCAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAGAGACCTGGTTAGACCAAGCCATTCCTTTCAAGT 420

QY 421 TATTAAGTCTGTGGTCACAAAAGACACTTATCTATGAAGAGGTTCTTTTATTC 480
DB 421 TATTAAGTCTGTGGTCACAAAAGACACTTATCTATGAAGAGGTTCTTTTATTC 480

QY 481 TTGCCAGTATATTTAGCTAACGATTTATGATGAGAGCAACACATATTTGATATT 540
DB 481 TTGCCAGTATATTTAGCTAACGATTTATGATGAGAGCAACACATATTTGATATT 540

QY 541 GTTCAATGATCTTCTAGGAGATTTGTTGGCTGCCAGCTCTCTGTCAAGAGCACA 600
DB 541 GTTCAATGATCTTCTAGGAGATTTGTTGGCTGCCAGCTCTCTGTCAAGAGCACA 600

QY 601 GGAATATATACCATGATCTACAGAACTTGGTAGTAGTCAATACAGAGAAATATCG 660
DB 601 GGAATATATACCATGATCTACAGAACTTGGTAGTAGTCAATACAGAGAAATATCG 660

QY 661 ACTCAGTACATCTGTGAGTGAAGACAGGTGTCACCTTGAAGGTTGGAGTGAAGAG 720
DB 661 ACTCAGTACATCTGTGAGTGAAGACAGGTGTCACCTTGAAGGTTGGAGTGAAGAG 720

QY 721 ACCTTGTACAGAGCTTACAGGAGAGAAACCTTCACTTTCATCTTTCATCTTTCAG 780
DB 721 ACCTTGTACAGAGCTTACAGGAGAGAAACCTTCACTTTCATCTTTCATCTTTCAG 780

QY 781 CTACCTCATCTAGAGGAGCAATTTAGTGAAGAGAGAAATTTAGATGAATTTATCTG 840
DB 781 CTACCTCATCTAGAGGAGCAATTTAGTGAAGAGAGAAATTTAGATGAATTTATCTG 840

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QY 841 GTGACGACAAAGAAAGCCACAAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC 900
DB 841 GTGACGACAAAGAAAGCCACAAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC 900

QY 901 TGGCTCTGTGTCTAATAAGGGAGATATCTTCTGAAGAACGACAGTACAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTCTAATAAGGGAGATATCTTCTGAAGAACGACAGTACAGTGAATCTACAG 960

QY 961 GGACGCCATCGAATCCGGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGGTTGG 1020
DB 961 GGACGCCATCGAATCCGGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGGTTGG 1020

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QY 1081 AAGATTATAGCCCTTGTGTAAGGACAAAGCTCTCAGATGAAGTATGATGAGGTATATC 1140
DB 1081 AAGATTATAGCCCTTGTGTAAGGACAAAGCTCTCAGATGAAGTATGATGAGGTATATC 1140

QY 1141 AAGTTACTGTGTATCAGGACGGGAGAGTATACAGATTCATTTGAAGAGATTCCTGAAA 1200
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DB 1621 CTGTGTGATTTGTCAAGTCCGACCTAAAATGTTTGCATTTGCCATGCGCAAAACAGGAC 1680

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QY 1801 AAGAGATTTATATTTCTTAACCTATATTAACCTTAGGAATTTAGACAACTGAAATTTAT 1860
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QY 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
DB 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920

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QY	1921	TCACCTACTTTGGTAGTGGAAATAGTGAATCTACTATATAATTTGGACTTGAATATGTAGCT	1980
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QY	1981	CATCCCTTTACACCAACTCTCAATTTTTAAATAAATTTCTACTCTCTCTTAAATGAGAAGTAC	2040
Db	1981	CATCCCTTTACACCAACTCTCAATTTTTAAATAAATTTCTACTCTCTCTTAAATGAGAAGTAC	2040
QY	2041	TTGGTTTTTTTTTTCTTTAAATATGATGACATTTAAATGTAACCTTATATTTTTTTTG	2100
Db	2041	TTGGTTTTTTTTTTCTTTAAATATGATGACATTTAAATGTAACCTTATATTTTTTTTG	2100
QY	2101	AGACCGAGCTTGTCTCTGTATACCCAGGCTCGAGTGCAGTGGGTGATCTTGGCTCACTGCA	2160
Db	2101	AGACCGAGCTTGTCTCTGTATACCCAGGCTCGAGTGCAGTGGGTGATCTTGGCTCACTGCA	2160
QY	2161	AGCTCTGCCCTCCCGGGTTCGCACACTTCTCTGCCCTCAGCCCTCCCAATTTAGCTTGGCC	2220
Db	2161	AGCTCTGCCCTCCCGGGTTCGCACCAATCTCTGCCCTCAGCCCTCCCAATTTAGCTTGGCC	2220
QY	2221	TACAGTCATCTGCCACACACACTTGGCTAAATTTTTTTGTACTTTTTTAGTAPAGACAGGGTTTC	2280
Db	2221	TACAGTCATCTGCCACACACACTTGGCTAAATTTTTTTGTACTTTTTTAGTAPAGACAGGGTTTC	2280
QY	2281	ACCGTGTTAGCCAGGATGGTCTGATCTCTGACTCTCTGATCCGCCACCTTCGSCCTCC	2340
Db	2281	ACCGTGTTAGCCAGGATGGTCTGATCTCTGACTCTCTGATCCGCCACCTTCGSCCTCC	2340
QY	2341	CAAACTGCTGGGATTTACAGGCATGAGCCACCG	2372
Db	2341	CAAACTGCTGGGATTTACAGGCATGAGCCACCG	2372

RESULT 4

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US-08-245-500A-2
Sequence 2, Application US/08245500A
Patent No. 5550023
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: BANNER, BIRCH, MCKTE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,500A
FILING DATE: 07-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid

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Db 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAAATTCAGATGAATATATCTG 840
 Qy 841 GTCAAGCACAAGAAAACCCACAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC 900
 Db 841 GTCAAGCACAAGAAAACCCACAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC 900
 Qy 901 TGGCTCTGTGTATTAAGGGAGATATCTTGTGAAGAACGAGTACGAGTGAATCTACAG 960
 Db 901 TGGCTCTGTGTATTAAGGGAGATATCTTGTGAAGAACGAGTACGAGTGAATCTACAG 960
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 Db 961 GGAGCCATCGAATCCGGATCTTGTGCTGGTGAAGTGAACATTCAGGTGATTTGGTGG 1020
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 Db 1021 ATCAGATTCAGTTCAGATCAGTTTACTGTAGATTTGAAGTGTGAATCTCTCGACTCAG 1080
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 Db 1321 ATAAAGGGAAATCTCTGAGAAGGCAAACTGGAAGAACTCAACAGCTGAAGAGGGCT 1380
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 Db 1381 TTGATGTTCTGATTTGAAAAAATCTAGTGAATGATTCAGAGATCATGTGTGGAGG 1440
 Qy 1441 AAAATGATGATAAAATCACAGCTTCACATCAAGAAAGTGAAGACTATTCTCAGC 1500
 Db 1441 AAAATGATGATAAAATCACAGCTTCACATCAAGAAAGTGAAGACTATTCTCAGC 1500
 Qy 1501 CATCACTTTCTAGTACATTTATAGCAGCCAGAGATGTCAGAGCTTTGAAGGG 1560
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 Qy 1561 AAGAAACCCAGACAAGAGAGTGTGGAATCTAGTTTCCCTTTAATGCCATTGAAC 1620
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 Db 1621 CTTGTGTGATTTGTCAGGTCGACCTTAAATGTTGCTATGTCATGCGCAAAACAGGAC 1680
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 Db 1681 ATCTTATGGCTGCTTTACATGTCGAAGAACTAAAGAAAGAAATGAGCCCTGCCAG 1740
 Qy 1741 TATGTAGACCAACCAATTCATGATTTGCTAACTTATTTCCCTTAGTTGACCTGTCTAT 1800
 Db 1741 TATGTAGACCAACCAATTCATGATTTGCTAACTTATTTCCCTTAGTTGACCTGTCTAT 1800
 Qy 1801 AAGAGATTTATATTTCTACTATATACCTAGCAATTTAGACAACCTGAATTTAT 1860
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 Qy 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATGATTTCTTCTTTAGTATAAT 1920
 Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATGATTTCTTCTTTAGTATAAT 1920

Qy 1921 TGACCTACTTTGGTAGTGAATAGTGAATACTTACTATATAATTGACTTGAATATGAGCT 1980
 Db 1921 TGACCTACTTTGGTAGTGAATAGTGAATACTTACTATATAATTGACTTGAATATGAGCT 1980
 Qy 1981 CATCTTTTACACCACTCTTAATTTAAATTTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 Db 1981 CATCTTTTACACCACTCTTAATTTAAATTTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 Qy 2041 TTGGTTTTTTTTTCTTAAATATATATATGACATTTAAATGTAACATTTATTTT 2100
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 Db 2161 AGCTCTGCGCTCCCGGGTTCGGACCATTTCTCTGCTCAGCTCCCATTTAGCTTGGCC 2220
 Qy 2221 TACAGTCTATCTGCCACCACTGCTGCTAAATTTTGTACTTTTGTAGAGACAGGTTTC 2280
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 Qy 2281 ACCGTGTTAGCCAGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTCGSCCTCC 2340
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 Db 2341 CAAAGTGTGGATTACAGGATGAGCCAGC 2372

RESULT 5
 US-08-390-546-2
 ; Sequence 2. Application US/08390546
 ; Patent No. 5606044
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; APPLICANT: HILL, DAVID E.
 ; APPLICANT: KINZLER, KENNETH W.
 ; APPLICANT: VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, version #1.25
 ; CURRENT APPLICATION DATA: US/08390,546
 ; FILING DATE: 07-APR-1993
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KAGAN, SARAH A.
 ; REGISTRATION NUMBER: 32,141
 ; REFERENCE/DOCKET NUMBER: 01107.42798
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-508-9100
 ; TELEFAX: 202-508-9299
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2372 base pairs


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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: CaCo-2
; POSITION IN GENOME:
; MAP POSITION: 12q12-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
; US-08-390-546-2

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Query Match          100.0%; Score 2372; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 781 CTACCTCATCTAGAGGAGGCAATTAGTGAGACAGAGAAATTCAGATGAATATATCTG 840

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Db 901 TGGCTCTGTGTGTAATAGGAGATATCTGTAAGAGCAGCAGTACAGTGAATCTACAG 960
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Db 1381 TTGATGTTCTGATTTGTAAGAACTATAGTGAATGATTCAGAGAGTGTGTTGAGG 1440
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Qy 1741 TATGTAGACACCAATTCATGATGCTGCTAATTTATTTCCCTAGTGTGACCTGCTAT 1800
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Qy 1801 AAGAGAAATATATATTTCTTAACATATATAACCTAGGAAATTTAGACAAACCTGAAAT 1860
Db 1801 AAGAGAAATATATATTTCTTAACATATATAACCTAGGAAATTTAGACAAACCTGAAAT 1860
Qy 1861 CACATATATCAAGAGTGAAGAAATGCTCAATTCATAGATTTCTTCTCTTTAGTATAT 1920

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Db 1861 CACATATATCAAAAGTGAGAAATGGCTCAATTCACATAGATTCTCTCTTTAGTATAAT 1920
Qy 1921 TGACCTACTTTGGTAGTGAATAGTAGTACTTACTATAATTTGACTTTGAATATGTAGCT 1980
Db 1921 TGACCTACTTTGGTAGTGAATAGTAGTACTTACTATAATTTGACTTTGAATATGTAGCT 1980
Qy 1981 CATCTTTACACAACTCTCTAAATTTTAAATATTTCTACTCTGTCTTAAATGAGAACTAC 2040
Db 1981 CATCTTTACACAACTCTCTAAATTTTAAATATTTCTACTCTGTCTTAAATGAGAACTAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGAACTTAAATTTTTTTTGG 2100
Db 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGAACTTAAATTTTTTTTGG 2100
Qy 2101 AGACCGAGTCTGCTCTGTATCCAGGCTGGAGTGCATGAGTGTCTTGGCTCAGTGA 2160
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Qy 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCCCTCAGCTCCCAATTTAGCTTGCC 2220
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Qy 2221 TAGAGTATCTGCCACACACCTGGCTAAATTTTTGTAATTTTGTAGTAGACAGGGTTTC 2280
Db 2221 TAGAGTATCTGCCACACACCTGGCTAAATTTTTGTAATTTTGTAGTAGACAGGGTTTC 2280
Qy 2281 ACCGTGTTAGCCAGGATGCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCCTCC 2340
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Qy 2341 CAAAGTCTGGGATTCAGCGGATGAGCCACCG 2372
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RESULT 6

US-08-390-479A-2

Sequence 2, Application US/08390479A

Patent No. 5618921

GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE

APPLICANT: HILL, DAVID E.

APPLICANT: KINZLER, KENNETH W.

APPLICANT: VOGELSTEIN, BERT

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDW2 GENE IN

TITLE OF INVENTION: HUMAN TUMORS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF, LTD.

STREET: 1001 G STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/390,479A

FILING DATE: 02-FEB-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.48992

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

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; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Homo sapiens
; CELL LINE: CaCo-2
; POSITION IN GENOME:
; MAP POSITION: 12q13-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
; US-08-390-479A-2

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Query Match 100.0%; Score 2372; DB 1; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCACCGCGCGAGCTTGGCTCTTCTGGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGA 60
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Db 61 GCAAGAAAGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Qy 121 CAGCCAGAGGACCGCTCCCTCCCGGATTTAGTCGCTGACGAGCGGCGGCGGCGGCGG 180
Db 121 CAGCCAGAGGACCGCTCCCTCCCGGATTTAGTCGCTGACGAGCGGCGGCGGCGGCGG 180
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Db 181 CAGAGTGGAAATGATCCCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
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Db 721 ACCTTGTAAGAGCTTCAGGAAAGAGAAACCTTTCATCTTTCACATTTGGTTTCTAGACCAT 780

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 Db 841 GTGAACGACAAAGAAACCGCCACAAATCTCATAGTATTTCCCTTTCCCTTTGATGAAGCC 900
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 Db 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGAATTTGAAAGTTGAATCTCTCGACTCAG 1080
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 Db 1081 AAGATTATAGCTTGTAGTGAAGAGCAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
 QY 1141 AAGTTACTGTGTATCAGGAGGAGAGTGTATACAGATTCATTTGAAGAGATCTCTGAAA 1200
 Db 1141 AAGTTACTGTGTATCAGGAGGAGAGTGTATACAGATTCATTTGAAGAGATCTCTGAAA 1200
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 Db 1201 TTTCTTACGTCATATTTGAAATGCACTTCATGCAATGAATGAATCCCTCCCTTCCAT 1260
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 Db 1261 CACATTCGAACAGATGTTGGGCCCTTCTGTGAGAAATTTGGCTTCTGGAAGATAAAGGAAA 1320
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 Db 1321 ATAAGGGGAATCTGAGAAAGCCAACTGAAACTCAACACAGCTGAAGGGCT 1380
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 Db 1381 TTGATGTTCCCTGATTGTAAGAACTATAGTGAATGATTTCCAGAGATCATGTGTTGAGG 1440
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 Db 1501 CATCAACTCTAGTAGCATTATTTATAGCAGCAAGAGATGTGAAGAGTTTGAAGGG 1560
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 Db 1741 TATGTAGCAACCAATTCATGCTGCTAACTTATTTCCCTTAGTTGACCTGCTCTAT 1800
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Db 1861 CACATATACAAAGTGAGAAATTCGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
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 Db 1921 TGACCTTACTTTGGTAGTGAATAGTACTTACTATAATTTGACTTGAATATGAGCT 1980
 QY 1981 CATCCTTTACACCAACTCCTAAATTTAAATTTTACTCTGTCTTTAAATGAGAAGTAC 2040
 Db 1981 CATCCTTTACACCAACTCCTAAATTTAAATTTTACTCTGTCTTTAAATGAGAAGTAC 2040
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 Db 2041 TTGGTTTTTTTCTTAAATATGATGACATTTAAATGTAATTTATTTTGTG 2100
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 Db 2101 AGACCGAGTCTTGGCTCTTTACCCAGGCTGGAGTGGCTGATCTTGGCTCACTGCA 2160
 QY 2161 AGCTCTGCCCTCCCGGGTTGCGACCATTTCTGCTCAGCCTCCCAATTAGCTTGGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTTGCGACCATTTCTGCTCAGCCTCCCAATTAGCTTGGCC 2220
 QY 2221 TACAGTCACTCTCCACACACACTGGCTAAATTTTGTACTTTTAGTAGACAGAGGTTTC 2280
 Db 2221 TACAGTCACTCTCCACACACACTGGCTAAATTTTGTACTTTTAGTAGACAGAGGTTTC 2280
 QY 2281 ACCGTGTTAGCAGAGATGCTCGATCTCCTGACCTGATCGGCTCCGCCCTCC 2340
 Db 2281 ACCGTGTTAGCAGAGATGCTCGATCTCCTGACCTGATCGGCTCCGCCCTCC 2340
 QY 2341 CAAAGTCTGGGATTACAGGATGAGCCACCG 2372
 Db 2341 CAAAGTCTGGGATTACAGGATGAGCCACCG 2372

RESULT 7
 US-08-557-393-2
 ; Sequence 2, Application US/08557393
 ; Patent No. 5702903
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; APPLICANT: HILL, DAVID E.
 ; APPLICANT: KINZLER, KENNETH W.
 ; APPLICANT: VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; TITLE OF INVENTION: HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/557,393
 ; FILING DATE: 13-NOV-1995
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/245,500
 ; FILING DATE: 18-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KAGAN, SARAH A.
 ; REGISTRATION NUMBER: 32,141
 ; REFERENCE/DOCKET NUMBER: 01107.42798
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-508-9100

1801 AAGAGAAATATATATTTCTTAACATATATAACCCCTAGGAATTTAGACAACCTGAAATTTATT 1860
1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
1921 TGACCTACTTTGGTAGTGAATAGTGAATACTTACTATAATTTGACTTGAATATGTAGCT 1980
1921 TGACCTACTTTGGTAGTGAATAGTGAATACTTACTATAATTTGACTTGAATATGTAGCT 1980
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1981 CATCCCTTACACCAACTCTTAATTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
2041 TTGGTTTTTTTTTCTTAATATGATATGACATTAATAATGTAACCTTATTTTGTG 2100
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2341 CAAAGTCTGGGATTCAGCATGAGCCACCG 2372

RESULT 8
US-08-390-516C-2
Sequence 2, Application US/08390516C
Patent No. 5708136
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,516C
FILING DATE: 07-APR-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-516C-2
Query Match 100.0%; Score 2372; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGCAGGCTTGGCTGCTTCTGGGGCTCTGTGGCCCTGTGTGGCCCTGTGTGCGAAAGATGA 60
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DB 1441 AAATGATGATAAATTCACAAAGCTTCACAAATCAGAAAGAGTGAAGTATCTCAGC 1500
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DB 1741 TATGTAGCAACCAATTCAGATGATGCTGCTAATCTATTTCCCTTACCTGACCTGCTAT 1800

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DB 1801 AAGAGAAATTAATATCTTAACCTATATATACCTAGAAATTTAGACAACTGAAATTTAT 1860
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DB 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
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DB 1981 CATCTTTTACACCACTCAATTTTAAATTAATTTCTACTCTGCTTAAATGAGAAGTAC 2040
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RESULT 9

US-08-390-517A-2
; Sequence 2, Application US/08390517A
; Patent No. 5736338
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDH2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,517A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-517A-2

Query Match		100.0%	Score 2372;	DB 1;	Length 2372;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 2372;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GCACCGCGGAGCTGGCTGCTCTGCGG	CGCTGTGCGGCCCTGTGTCGGAAGATGGA	60	
Db	1	GCACCGCGGAGCTGGCTGCTCTGCGG	CGCTGTGCGGCCCTGTGTCGGAAGATGGA	60	
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Db	61	GCAAGAGCGGAGCGCGGCGCGCGCG	CGACCCCTCTGACCGAGATCCCTGCTGCTTCG	120	
Qy	121	CAGCAGGAGCAGCTCCCTCCCGGAT	TAGTGGTACGAGCGCCAGTGGCCCGC	180	
Db	121	CAGCAGGAGCAGCTCCCTCCCGGAT	TAGTGGTACGAGCGCCAGTGGCCCGC	180	
Qy	181	GAGAGTGAATATCCCGAGCGCCAG	GGCGTGTGCTCCCGAGTAGTCCCGGTG	240	
Db	181	GAGAGTGAATATCCCGAGCGCCAG	GGCGTGTGCTCCCGAGTAGTCCCGGTG	240	
Qy	241	AAGGAACTGGGAGCTTTGAGGAC	CCCGGACTCCCAAGCGGAAACCCCGGATGGTGA	300	
Db	241	AAGGAACTGGGAGCTTTGAGGAC	CCCGGACTCCCAAGCGGAAACCCCGGATGGTGA	300	
Qy	301	GGAGCAGGAAATGTCATACCAAT	GTCTGTACCTACTGATGTGCTGTAAACCACT	360	
Db	301	GGAGCAGGAAATGTCATACCAAT	GTCTGTACCTACTGATGTGCTGTAAACCACT	360	
Qy	361	CACAGATTCGAGCTTCGGAAC	AGAGCCCTGGTTAGACCAAGACONTTGTCTTTGAAAT	420	
Db	361	CACAGATTCGAGCTTCGGAAC	AGAGCCCTGGTTAGACCAAGACONTTGTCTTTGAAAT	420	
Qy	421	TATTAAAGTCTGTGGTGCACAA	AGACACTTATCTATGAAGAGGTTCTTTTATC	480	
Db	421	TATTAAAGTCTGTGGTGCACAA	AGACACTTATCTATGAAGAGGTTCTTTTATC	480	
Qy	481	TGGCCAGTATATATGACTAA	CAACGATATATGATGAGAACCAACATATATGATAT	540	
Db	481	TGGCCAGTATATATGACTAA	CAACGATATATGATGAGAACCAACATATATGATAT	540	
Qy	541	GTTCAAAATGATCTCTAGGAG	ATTTGTTGGCGTGGCAAGCTTCTCTGTGAAAGAGCACA	600	
Db	541	GTTCAAAATGATCTCTAGGAG	ATTTGTTGGCGTGGCAAGCTTCTCTGTGAAAGAGCACA	600	
Qy	601	GGAAATATATACCATGATCT	ACAGGAACCTTGGTAGTACATACAGGAGATCATGG	660	
Db	601	GGAAATATATACCATGATCT	ACAGGAACCTTGGTAGTACATACAGGAGATCATGG	660	
Qy	661	ACTCAGGTACATCTGTGAGT	GAGAACAGGTGTCACTTGAAGTGGGAGTGATCAAAAGG	720	
Db	661	ACTCAGGTACATCTGTGAGT	GAGAACAGGTGTCACTTGAAGTGGGAGTGATCAAAAGG	720	

Db	661	ACTCAGGTACATCTGTGAGT	GAGAACAGGTGTCACTTGAAGTGGGAGTGATCAAAAGG	720
Qy	721	ACCTTGTACAAAGAGCTT	CAGGAAGAGAAACCTTCATCTTCACATTTGGTTCTTAGACCAT	780
Db	721	ACCTTGTACAAAGAGCTT	CAGGAAGAGAAACCTTCATCTTCACATTTGGTTCTTAGACCAT	780
Qy	781	CTACCTCATCTAGAAGG	AGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTG	840
Db	781	CTACCTCATCTAGAAGG	AGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTG	840
Qy	841	GTGAACGACAAAGAAAC	CGCCACAAATCTGATAGTATTTCCCTTTCTTTGATGAAAGCC	900
Db	841	GTGAACGACAAAGAAAC	CGCCACAAATCTGATAGTATTTCCCTTTCTTTGATGAAAGCC	900
Qy	901	TGGCTCTGTGTAAATA	AGGGAGATATGTTGTGAAAGAGCAGTAGCAGTGAATCTACAG	960
Db	901	TGGCTCTGTGTAAATA	AGGGAGATATGTTGTGAAAGAGCAGTAGCAGTGAATCTACAG	960
Qy	961	GGACGCCATCGAAT	CCGGATCTTGTGATGCTGGTGTAAAGTTGAATCTCTCGACTCAG	1020
Db	961	GGACGCCATCGAAT	CCGGATCTTGTGATGCTGGTGTAAAGTTGAATCTCTCGACTCAG	1020
Qy	1021	ATCAGGATTCAGTT	CAGATCAGTTTGTAGTAGAATTTGAAGTTGAATCTCTCGACTCAG	1080
Db	1021	ATCAGGATTCAGTT	CAGATCAGTTTGTAGTAGAATTTGAAGTTGAATCTCTCGACTCAG	1080
Qy	1081	AAGATTATACCTT	AGTGAAGGACAACTCTCAGATGAGATGATGATATC	1140
Db	1081	AAGATTATACCTT	AGTGAAGGACAACTCTCAGATGAGATGATGATATC	1140
Qy	1141	AAGTTACTGTCT	ATCAGGCGGAGAGTGATACAGATTCATTTGAAGAGATCCCTGAAA	1200
Db	1141	AAGTTACTGTCT	ATCAGGCGGAGAGTGATACAGATTCATTTGAAGAGATCCCTGAAA	1200
Qy	1201	TTTCCTTAGCTG	ACTTATGGAATGCACTTTCATGCAATGAAATGAAATCCCTCCCTCCAT	1260
Db	1201	TTTCCTTAGCTG	ACTTATGGAATGCACTTTCATGCAATGAAATGAAATCCCTCCCTCCAT	1260
Qy	1261	CACATTCGAACAGAT	GTGGGCCCTTCGTGAGATTTGGCTTCTTGAAGATTAAGGGAAG	1320
Db	1261	CACATTCGAACAGAT	GTGGGCCCTTCGTGAGATTTGGCTTCTTGAAGATTAAGGGAAG	1320
Qy	1321	ATAAGGGGAAATCT	CTGAGAAAGCCAACTGGAAGCTCAACACAAAGCTGAAGAGGGCT	1380
Db	1321	ATAAGGGGAAATCT	CTGAGAAAGCCAACTGGAAGCTCAACACAAAGCTGAAGAGGGCT	1380
Qy	1381	TTGATGTTCTG	TGATTTAAAGAACTATAGTGAATGATTCAGAGAGTCTATGTTGAGG	1440
Db	1381	TTGATGTTCTG	TGATTTAAAGAACTATAGTGAATGATTCAGAGAGTCTATGTTGAGG	1440
Qy	1441	AAAATGATGATA	AAAAATCACAAAGCTTCACAAATCACAAAGAAAGTGAAGACTATTTCTCAGC	1500
Db	1441	AAAATGATGATA	AAAAATCACAAAGCTTCACAAATCACAAAGAAAGTGAAGACTATTTCTCAGC	1500
Qy	1501	CATCAACTTCT	AGTATGATTTATAGCAGCAAGAAAGATGTGAAAGAGTTTGAAGGG	1560
Db	1501	CATCAACTTCT	AGTATGATTTATAGCAGCAAGAAAGATGTGAAAGAGTTTGAAGGG	1560
Qy	1561	AAGAAACCCAG	ACAAAGAGAGTGGATCTAGTTTGGCCCTTAATGCCATTAAC	1620
Db	1561	AAGAAACCCAG	ACAAAGAGAGTGGATCTAGTTTGGCCCTTAATGCCATTAAC	1620
Qy	1621	CTTGTGTGATTT	GTCAAGGTCGACCTTCAAAATGTTGCTATTTGCCATGGCAAAACAGGAC	1680
Db	1621	CTTGTGTGATTT	GTCAAGGTCGACCTTCAAAATGTTGCTATTTGCCATGGCAAAACAGGAC	1680
Qy	1681	ATCTTATGGCC	TCTTTTACATGTGCAAGAAAGCTAAAGAAAGAAATTAAGCCTGCCAG	1740
Db	1681	ATCTTATGGCC	TCTTTTACATGTGCAAGAAAGCTAAAGAAAGAAATTAAGCCTGCCAG	1740
Qy	1741	TATGTAGAACCA	CAATTCATGATTTGCTAACTTATTTCCCTTAGTTCACCTGCTAT	1800
Db	1741	TATGTAGAACCA	CAATTCATGATTTGCTAACTTATTTCCCTTAGTTCACCTGCTAT	1800

Qy 1801 AAGAGATTATATATTTCTTAACCTATATTAACCCCTAGGAATTTAGACAACCTGAAATTTATT 1860
Db 1801 AAGAGATTATATATTTCTTAACCTATATTAACCCCTAGGAATTTAGACAACCTGAAATTTATT 1860
Qy 1861 CACATATATCAAAAGTCAGAAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
Db 1861 CACATATATCAAAAGTCAGAAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
Qy 1921 TGACCTACTTTGTAGTGAATAGTGAATAGTACTATATTAATTTGACTTGAATTTAGT 1980
Db 1921 TGACCTACTTTGTAGTGAATAGTGAATAGTACTATATTAATTTGACTTGAATTTAGT 1980
Qy 1981 CATCCTTTACACCAACTCTTAATTTTAAATAATTTCTACTCTGTCTTTAAATGAGAAGTAC 2040
Db 1981 CATCCTTTACACCAACTCTTAATTTTAAATAATTTCTACTCTGTCTTTAAATGAGAAGTAC 2040
Qy 2041 TTGGTTTCTTTCTTAATATATATATGACATTTAAATGTAATTTATTTTCTTTTCTG 2100
Db 2041 TTGGTTTCTTTCTTAATATATATATGACATTTAAATGTAATTTATTTTCTTTTCTG 2100
Qy 2101 AGACCGAGTCTTCTCTGTTTACCCAGGCTGGAGTGCAGTGGTGATCTTGGCTCACTGCA 2160
Db 2101 AGACCGAGTCTTCTCTGTTTACCCAGGCTGGAGTGCAGTGGTGATCTTGGCTCACTGCA 2160
Qy 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCTCAGCCCTCCCAATTTAGCTTGGCC 2220
Db 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCTCAGCCCTCCCAATTTAGCTTGGCC 2220
Qy 2221 TACAGTCATCTGCCACACACCTGGCTAAATTTTGTACTTTTGTAGTACAGACAGGGTTTC 2280
Db 2221 TACAGTCATCTGCCACACACCTGGCTAAATTTTGTACTTTTGTAGTACAGACAGGGTTTC 2280
Qy 2281 ACCGTGTTAGCAGGATGTCGTGATCTCTGACCTCGTGATCGCGCCACCTCGGGCTCC 2340
Db 2281 ACCGTGTTAGCAGGATGTCGTGATCTCTGACCTCGTGATCGCGCCACCTCGGGCTCC 2340
Qy 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372

RESULT 10
US-08-390-515A-2
: Sequence 2, Application US/08390515A
: Patent No. 5756455
: GENERAL INFORMATION:
: APPLICANT: BURRELL, MARILEE
: APPLICANT: HILL, DAVID E.
: APPLICANT: KINZLER, KENNETH W.
: APPLICANT: VOGELSTEIN, BERT
: TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDW2 GENE IN
: TITLE OF INVENTION: HUMAN TUMORS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
: STREET: 1001 G STREET, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20001
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/390,515A
: FILING DATE: 07-APR-1993
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: KAGAN, SARAH A.
: REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-515A-2
Query Match 100.0%; Score 2372; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCACCCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGCTCGGAAAGATGGA 60
Db 1 GCACCCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGCTCGGAAAGATGGA 60
Qy 61 GCAAGAAGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 61 GCAAGAAGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Qy 121 CAGCCAGGAGCACCCTCCCTCCCGGATTTAGTGGTACGAGCGCCAGTGCCTGGCCCG 180
Db 121 CAGCCAGGAGCACCCTCCCTCCCGGATTTAGTGGTACGAGCGCCAGTGCCTGGCCCG 180
Qy 181 GAGAGTGAATGATATCCCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 181 GAGAGTGAATGATATCCCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Qy 241 AAGGAACTGGGAGTCTTGGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 241 AAGGAACTGGGAGTCTTGGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Qy 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACCTACTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Db 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACCTACTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Qy 361 CACAGATTTCCAGCTTCGGAAACAGAGAGCGCTGGTTAGACCAAGCCCATTCCTTTTGAAGT 420
Db 361 CACAGATTTCCAGCTTCGGAAACAGAGAGCGCTGGTTAGACCAAGCCCATTCCTTTTGAAGT 420
Qy 421 TATTAAGTCTGTGTGTGCACAAAAGACACTATATCTATCTATCTATCTATCTATCTATCTATCTATCT 480
Db 421 TATTAAGTCTGTGTGTGCACAAAAGACACTATATCTATCTATCTATCTATCTATCTATCTATCTATCT 480
Qy 481 TTGGCCAGTATATTTATGACTAAACGATTTATGATGAGAGCAACACATATTTGTATTT 540
Db 481 TTGGCCAGTATATTTATGACTAAACGATTTATGATGAGAGCAACACATATTTGTATTT 540
Qy 541 GTTCAATGATCTCTAGGAGATTTGTTGGCGTCCCAAGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 541 GTTCAATGATCTCTAGGAGATTTGTTGGCGTCCCAAGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy 601 GGAATATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAGCAGCAATCATCGG 660
Db 601 GGAATATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAGCAGCAATCATCGG 660
Qy 661 ACTCAGGTACATCTGTGAGTGAACACAGGTGTACCTTTGAAAGGTGGGAGTGAATCAAAAGG 720

Db 661 ACTCAGTACATCTGTGAGTCAGACAGGTCACCTTGAAGTGGAGTGATCAAAAGG 720
 QY 721 ACCTTGACAGAGCTTCAGAGAGAAACCTTCATCTTCACATTTGGTTCTAGACCAAT 780
 Db 721 ACCTTGACAGAGCTTCAGAGAGAAACCTTCATCTTCACATTTGGTTCTAGACCAAT 780
 QY 781 CTACCTTCATCTAGAGAGAGCAATTTAGTGAGACAGAAAGAAATTCAGATGAATATCTG 840
 Db 781 CTACCTTCATCTAGAGAGAGCAATTTAGTGAGACAGAAAGAAATTCAGATGAATATCTG 840
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 Db 841 GTGACGCAAAAGAAACCGCACAAATCTGATAGTATTTCCCTTCCTTTGATGAAGCC 900
 QY 901 TGGCTCTGTGTAAAGGAGAGATATGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 Db 901 TGGCTCTGTGTAAAGGAGAGATATGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 QY 961 GGAGCCCATCGAATCGGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGTTGG 1020
 Db 961 GGAGCCCATCGAATCGGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGTTGG 1020
 QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
 Db 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
 QY 1081 AAGATTTATAGCTTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 Db 1081 AAGATTTATAGCTTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 QY 1141 AAGTTACTGTATCAGCAGGAGAGAGATGATACAGATTCATTGTAAGAGAGATTCCTGAAA 1200
 Db 1141 AAGTTACTGTATCAGCAGGAGAGAGATGATACAGATTCATTGTAAGAGAGATTCCTGAAA 1200
 QY 1201 TTTCCCTTACTGACTATTTGGAATGCACTTCATGCAATGAATGAATGCAATGCAATGCAAT 1260
 Db 1201 TTTCCCTTACTGACTATTTGGAATGCACTTCATGCAATGAATGAATGCAATGCAATGCAAT 1260
 QY 1261 CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATTCCTTCCTGAGAGATTAAGAGGAAAG 1320
 Db 1261 CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATTCCTTCCTGAGAGATTAAGAGGAAAG 1320
 QY 1321 ATAAAGGGAATCTCTGAGAAAGCAAACTGGAAGAACTCAACAGAGCTGAAGAGGGCT 1380
 Db 1321 ATAAAGGGAATCTCTGAGAAAGCAAACTGGAAGAACTCAACAGAGCTGAAGAGGGCT 1380
 QY 1381 TTGATGTTCTGATGTAAGAAACTATAGTGAATGATTCAGAGAGTCAATGTTGGAG 1440
 Db 1381 TTGATGTTCTGATGTAAGAAACTATAGTGAATGATTCAGAGAGTCAATGTTGGAG 1440
 QY 1441 AAAATGATGTAAGAAACTATAGTGAATGATTCAGAGAGTCAATGTTGGAG 1500
 Db 1441 AAAATGATGTAAGAAACTATAGTGAATGATTCAGAGAGTCAATGTTGGAG 1500
 QY 1501 CATCAACTTCTAGTACGATTTATAGCAGCAAGAGAGATGTAAGAGATTTGAAAGGG 1560
 Db 1501 CATCAACTTCTAGTACGATTTATAGCAGCAAGAGAGATGTAAGAGATTTGAAAGGG 1560
 QY 1561 AAGAAACCAAGCAAGAGAGAGATGTTGGAATCTAGTTTGGCCCTTAAATGCCATTGAAC 1620
 Db 1561 AAGAAACCAAGCAAGAGAGAGATGTTGGAATCTAGTTTGGCCCTTAAATGCCATTGAAC 1620
 QY 1621 CTGCTGATTTGTCAGAGTCACTTAAATGTTGATGATTCATGTCGCAAGAGAGAGAG 1680
 Db 1621 CTGCTGATTTGTCAGAGTCACTTAAATGTTGATGATTCATGTCGCAAGAGAGAGAGAG 1680
 QY 1681 ATCTTATGCTGCTTTACATGTCAGAAAGAGCTTAAAGAAAGAGATTAAGCCTGCCCCAG 1740
 Db 1681 ATCTTATGCTGCTTTACATGTCAGAAAGAGCTTAAAGAAAGAGATTAAGCCTGCCCCAG 1740
 QY 1741 TATGTAGACCAACCAATTCATGATTTGCTTAACCTTATTTCCCTTAGTTCACCTGCTAT 1800

Db 1741 TATGTAGACCAACCAATTCATGATTTGCTTAACCTTATTTCCCTTAGTTCACCTGCTAT 1800
 QY 1801 AAGAGATATATATTTCTTAACCTATATACCTAGGATTTAGACACCTGAATTTAT 1860
 Db 1801 AAGAGATATATATTTCTTAACCTATATACCTAGGATTTAGACACCTGAATTTAT 1860
 QY 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 Db 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 QY 1921 TGACCTTACCTTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 Db 1921 TGACCTTACCTTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 QY 1981 CATCTTTACACCAACTCTCTTAAATGATGATGATGATGATGATGATGATGATGATGAT 2040
 Db 1981 CATCTTTACACCAACTCTCTTAAATGATGATGATGATGATGATGATGATGATGATGAT 2040
 QY 2041 TTTGGTTTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 Db 2041 TTTGGTTTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 QY 2101 AGACCGAGTCTGCTCTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTGCTCTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 QY 2161 AGCTCTGCTCTCCCGGTTCCGACCATTCCTGCTGATCGGCTCCCAATAGCTTGGCC 2220
 Db 2161 AGCTCTGCTCTCCCGGTTCCGACCATTCCTGCTGATCGGCTCCCAATAGCTTGGCC 2220
 QY 2221 TACAGTCACTGCTCCACACACCTGGCTAATTTTGTACTTTTAGTAGACAGAGGTTTC 2280
 Db 2221 TACAGTCACTGCTCCACACACCTGGCTAATTTTGTACTTTTAGTAGACAGAGGTTTC 2280
 QY 2281 ACCGTGTTAGCAGAGTGTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGAT 2340
 Db 2281 ACCGTGTTAGCAGAGTGTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGAT 2340
 QY 2341 CAAAGTCTGGGATTTACAGGCATGAGCCACCG 2372
 Db 2341 CAAAGTCTGGGATTTACAGGCATGAGCCACCG 2372

RESULT 11
 US-08-801-718-2
 ; Sequence 2, Application US/08801718
 ; Patent No. 5858976
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; APPLICANT: HILL, DAVID E.
 ; APPLICANT: KINZLER, KENNETH W.
 ; APPLICANT: VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; TITLE OF INVENTION: HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/801,718
 ; FILING DATE: 14-FEB-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION NUMBER: 08/390,515

;; FILING DATE: 07-APR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KAGAN, SARAH A.
;; REGISTRATION NUMBER: 32,141
;; REFERENCE/DOCKET NUMBER: 01107.42798
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-508-9100
;; TELEFAX: 202-508-9299
;; TELEX: 197430 BBMB UT
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2372 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; CELL LINE: CrCo-2
;; POSITION IN GENOME: 12q12-14
;; MAP POSITION:
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 312..1784
;; US-08-801-718-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCTGTCGGAAGATGGA 60
DB 1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCTGTCGGAAGATGGA 60
QY 61 GCAGAGCGGAGCGCGGAGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
DB 61 GCAGAGCGGAGCGCGGAGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
QY 121 CAGCCAGGAGCAGCGCTCCCTCCCGGATAGTGGCTAGCAGCGCCGACGTCCTGCGCCG 180
DB 121 CAGCCAGGAGCAGCGCTCCCTCCCGGATAGTGGCTAGCAGCGCGCCGACGTCCTGCGCCG 180
QY 181 GAGAGTGGATGATCCCCGAGCGCCGAGCGCTGCTGCTCCGAGTAGTAGTCCCGCTG 240
DB 181 GAGAGTGGATGATCCCCGAGCGCCGAGCGCTGCTGCTCCGAGTAGTAGTCCCGCTG 240
QY 241 AAGAAACTGGGAGTCTTGGAGGACCCCGGACTCCAGCGGAAACCCCGGATGGTGA 300
DB 241 AAGAAACTGGGAGTCTTGGAGGACCCCGGACTCCAGCGGAAACCCCGGATGGTGA 300
QY 301 GGAGCAGCAATGTGCAATACCAATCTCTGTACCTACTGATGGTGTGCTGAACCACT 360
DB 301 GGAGCAGCAATGTGCAATACCAATCTCTGTACCTACTGATGGTGTGCTGAACCACT 360
QY 361 CACAGATTCAGCTTCGGAACAGAGACCCCTGGTTAGACCAAGCAATGCTTTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAGAGACCCCTGGTTAGACCAAGCAATGCTTTTGAAGT 420
QY 421 TATTAAAGTCTGTGGTGCACAAAAGACACTTATACATGAAAGAGGTTCTTTTATC 480
DB 421 TATTAAAGTCTGTGGTGCACAAAAGACACTTATACATGAAAGAGGTTCTTTTATC 480
QY 481 TTGGCCAGTATATATGACTAAACGATATATGATGAGAGCAACACATATGATATT 540
DB 481 TTGGCCAGTATATATGACTAAACGATATATGATGAGAGCAACACATATGATATT 540
QY 541 GTTCAATGATCTCTAGGAGATTTGTTGGCTGCCAAGCTTCTCTGTGAAAGAGCACA 600
DB 541 GTTCAATGATCTCTAGGAGATTTGTTGGCTGCCAAGCTTCTCTGTGAAAGAGCACA 600
QY 601 GGAATATATATACCATGATCTACAGGAAGCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660

DB 601 GGAATATATATACCATGATCTACAGGAAGCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
QY 661 ACTCAGGTACATCTGTGAGTGAGAACACAGGTGTACCTTGAAGGTGGAGTGATCAAAAGG 720
DB 661 ACTCAGGTACATCTGTGAGTGAGAACACAGGTGTACCTTGAAGGTGGAGTGATCAAAAGG 720
QY 721 ACCTTGTACAAGAGCTTTCAGGAAGAGAAACCTTCATCTTACATTTGGTTCTTAGACCAT 780
DB 721 ACCTTGTACAAGAGCTTTCAGGAAGAGAAACCTTCATCTTACATTTGGTTCTTAGACCAT 780
QY 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
DB 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
QY 841 GTGAAGCACAAGAAACGCCACAAATCTGTAGTAGTATTTCCCTTTTCCCTTTGATGAAAGCC 900
DB 841 GTGAAGCACAAGAAACGCCACAAATCTGTAGTAGTATTTCCCTTTTCCCTTTGATGAAAGCC 900
QY 901 TGGCTCTGTGTGTAATAAGGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTGTAATAAGGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
QY 961 GGACGCCATCGAATCCGGATCTTGTATGCTGTGTGAAGTGAACATTCAGGTGATGTTGG 1020
DB 961 GGACGCCATCGAATCCGGATCTTGTATGCTGTGTGAAGTGAACATTCAGGTGATGTTGG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAGTAATTTGAAGTTGCAATCTCTGACTCAG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAGTAATTTGAAGTTGCAATCTCTGACTCAG 1080
QY 1081 AAGATTATAGCCCTTGTGAGGAAGGACAACTCTCAGATGAAAGATGATGAGTATATC 1140
DB 1081 AAGATTATAGCCCTTGTGAGGAAGGACAACTCTCAGATGAAAGATGATGAGTATATC 1140
QY 1141 AAGTTACTGTGTATCAGCGGAGAGTATACAGATTCATTTGAGAGATCCTGAAA 1200
DB 1141 AAGTTACTGTGTATCAGCGGAGAGTATACAGATTCATTTGAGAGATCCTGAAA 1200
QY 1201 TTTCTTGTAGTACTATTGGAATGCACCTTCATGCAATGAAATGAAATGAAATGAAATGAAAT 1260
DB 1201 TTTCTTGTAGTACTATTGGAATGCACCTTCATGCAATGAAATGAAATGAAATGAAATGAAAT 1260
QY 1261 CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGCTTCCCTGAGATGAAAGGAAAG 1320
DB 1261 CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGCTTCCCTGAGATGAAAGGAAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAACTCAACAACTCAACAACT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAACTCAACAACTCAACAACT 1380
QY 1381 TTGATGTTCTGTGATTTGTAATAAACTATAGTGAATGATTCCAGAGAGTATGTTCTGAGG 1440
DB 1381 TTGATGTTCTGTGATTTGTAATAAACTATAGTGAATGATTCCAGAGAGTATGTTCTGAGG 1440
QY 1441 AAAATGATGATAAATTCACAAAGCTTCAATCAACAAAGAGTGAAGAGTATTTCTCAGC 1500
DB 1441 AAAATGATGATAAATTCACAAAGCTTCAATCAACAAAGAGTGAAGAGTATTTCTCAGC 1500
QY 1501 CATCAACTCTCTAGTACATTTATATAGCAGCAAGAGAGTGTGAAGAGTGTGAAAGGG 1560
DB 1501 CATCAACTCTCTAGTACATTTATATAGCAGCAAGAGAGTGTGAAGAGTGTGAAAGGG 1560
QY 1561 AAGAAACCCAGCAAGAGAGAGTGTGAATCTAGTTTGGCCCTTTAATGCCATTTGAAC 1620
DB 1561 AAGAAACCCAGCAAGAGAGAGTGTGAATCTAGTTTGGCCCTTTAATGCCATTTGAAC 1620
QY 1621 CTTCTGTGATTTGTCAGGTCGACCTTAAATGTTGATTTGCCATGGCAAAACAGAC 1680
DB 1621 CTTCTGTGATTTGTCAGGTCGACCTTAAATGTTGATTTGCCATGGCAAAACAGAC 1680
QY 1681 ATCTTATGGCCCTGCTTTACATGTGCAAGAGCTTAAAGAAAGGAATTAAGCCCTGCCCCAG 1740
DB 1681 ATCTTATGGCCCTGCTTTACATGTGCAAGAGCTTAAAGAAAGGAATTAAGCCCTGCCCCAG 1740

Db 1691 ATCTATGGCGCTGTTTACATGTGCAAGAAGCTAAAGAAAAAGAAATAAGCCCTGCCAG 1740
Qy 1741 TATGTAGAACCAACCAATTAATGATGCTAATCTATTTATTTCCCTAGTTGACCTGCTCTAT 1800
Db 1741 TATGTAGAACCAACCAATTAATGATGCTAATCTATTTATTTCCCTAGTTGACCTGCTCTAT 1800
Qy 1801 AAGAGAAATATATATTTCTAATCTATATAACCCCTAGGAATTTAGACAACCTGAATATAT 1860
Db 1801 AAGAGAAATATATATTTCTAATCTATATAACCCCTAGGAATTTAGACAACCTGAATATAT 1860
Qy 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
Qy 1921 TGACCTACTTTGGTGGGAATAGTGAATCTATATATTTGACTTGAATATAGTACT 1980
Db 1921 TGACCTACTTTGGTGGGAATAGTGAATCTATATATTTGACTTGAATATAGTACT 1980
Qy 1981 CATCTTTTACACCAACCTCCTAAATTTTAAATATTTTCTACTCTGCTTAAATGAGAAGTAC 2040
Db 1981 CATCTTTTACACCAACCTCCTAAATTTTAAATATTTTCTACTCTGCTTAAATGAGAAGTAC 2040
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Db 2101 AGACCGAGTCTTGCTGTTTACCCAGGCTGGAGTGCAGTGGTGTATCTTGGCTCACTGCA 2160
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Qy 2221 TACAGTCACTGCGCACCACTTGGCTGCTTAAATTTTCTACTTTTAGTAGACAGGGTTTC 2280
Db 2221 TACAGTCACTGCGCACCACTTGGCTGCTTAAATTTTCTACTTTTAGTAGACAGGGTTTC 2280
Qy 2281 ACCGTGTTAGCAGGATGGTCTGATCTGCTGACCTCGTGATCCGCCACCTCGGCCCTCC 2340
Db 2281 ACCGTGTTAGCAGGATGGTCTGATCTGCTGACCTCGTGATCCGCCACCTCGGCCCTCC 2340
Qy 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372

RESULT 12

US-09-073-567-1
; Sequence 1, Application US/09073567
; Patent No. 6013786
; GENERAL INFORMATION:
; APPLICANT: Jiaodong Chen
; APPLICANT: Sudhir Agrawal
; APPLICANT: Rulwen Zhang
; TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,567
; FILING DATE:
; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield, Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 98,057-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: hmdm2 DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-073-567-1

Query Match 100.0%; Score 2372; DB 3; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCGGAGCTTGGCTCTCTGGGGCTGTGTGGCCCTGTGTGTCGGAAAGATGA 60
Db 1 GCACCGCGGAGCTTGGCTCTCTGGGGCTGTGTGGCCCTGTGTGTCGGAAAGATGA 60
Qy 61 GCAAGAAGCCGAGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 61 GCAAGAAGCCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Qy 121 CAGCCAGGAGCAGCGTCCCTCCCGGATTTAGTGGGTACGAGCGCCCGAGTGGCCCG 180
Db 121 CAGCCAGGAGCAGCGTCCCTCCCGGATTTAGTGGGTACGAGCGCCCGAGTGGCCCG 180
Qy 181 GAGAGTGAATGATCCCGAGGCGCCAGGGGCTGTGTCCCGAGTAGTCAGTCCCGGTG 240
Db 181 GAGAGTGAATGATCCCGAGGCGCCAGGGGCTGTGTCCCGAGTAGTCAGTCCCGGTG 240
Qy 241 AAGGAACTGGGGAGCTTTGAGGAGCCCCCGACTCCAAGCGGAAAAACCCCGGATGGTA 300
Db 241 AAGGAACTGGGGAGCTTTGAGGAGCCCCCGACTCCAAGCGGAAAAACCCCGGATGGTA 300
Qy 301 GGAGCAGGCAATGTGCAATACCAACATGTGTACTGTACTGTGTGTGTGTGTGTGTGTGT 360
Db 301 GGAGCAGGCAATGTGCAATACCAACATGTGTACTGTACTGTGTGTGTGTGTGTGTGT 360
Qy 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTCCTTTTGAAT 420
Db 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTCCTTTTGAAT 420
Qy 421 TATTAAAGTCTGTGGTGCACAAAAAGACACTTATATCTATGAAGAGGTTCTTTTATC 480
Db 421 TATTAAAGTCTGTGGTGCACAAAAAGACACTTATATCTATGAAGAGGTTCTTTTATC 480
Qy 481 TTGGCCAGTATATATGACTAAACGATTTATATGATGAGAAGCAACACATATTTATAT 540
Db 481 TTGGCCAGTATATATGACTAAACGATTTATATGATGAGAAGCAACACATATTTATAT 540
Qy 541 GTTCAATGATCTTCTAGGAGATTTGTTGGCGGCCAACCTTCTCTGTGAAGAGACACA 600
Db 541 GTTCAATGATCTTCTAGGAGATTTGTTGGCGGCCAACCTTCTCTGTGAAGAGACACA 600
Qy 601 GGAAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATATCGG 660
Db 601 GGAAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATATCGG 660
Qy 661 ACTCAGGTACATCTCTGAGTGCAGAACAGGTGTACCTTTGAAGTGGGAGTGCATCAAGG 720
Db 661 ACTCAGGTACATCTCTGAGTGCAGAACAGGTGTACCTTTGAAGTGGGAGTGCATCAAGG 720
Qy 721 ACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCAATTTGGTTCTTAGACCAT 780
Db 721 ACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCAATTTGGTTCTTAGACCAT 780

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2372 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Unknown

; ANTI-SENSE: NO

; PUBLICATION INFORMATION:

; AUTHORS: Oliner, J. D.

; AUTHORS: Kinzler, K. W.

; AUTHORS: Meltzer, P. S.

; AUTHORS: George, D. L.

; AUTHORS: Vogelstein, B.

; TITLE: Amplification of a gene encoding a

; TITLE: p53-associated protein in human sarcomas

; JOURNAL: Nature

; VOLUME: 358

; ISSUE: 6381

; PAGES: 80-83

; DATE: 02-JUL-1992

; US-09-280-805-1

Query Match 100.0%; Score 2372; DB 4; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60

DB 1 GCACCGCGGAGCTTGGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60

QY 61 GCAGAGCCGAGCCGAGGGGGGGGACCCCTCTGACCGAGATCCTGCTGTTTCG 120

DB 61 GCAAGAAGCCGAGCCGAGGGGGGGGACCCCTCTGACCGAGATCCTGCTGTTTCG 120

QY 121 CAGCAGGAGCAGCCGCTCCCTCCCGGATTAGTGCCTACAGCGCCGACGTCGCCCTGGCCCG 180

DB 121 CAGCAGGAGCAGCCGCTCCCTCCCGGATTAGTGCCTACAGCGCCGACGTCGCCCTGGCCCG 180

QY 181 GAGAGTGAATGATCCCGAGGCGCCAGGGCGTGTGCTTCCCGAGTAGTCAGTCCCGCG 240

DB 181 GAGAGTGAATGATCCCGAGGCGCCAGGGCGTGTGCTTCCCGAGTAGTCAGTCCCGCG 240

QY 241 AAGAAATCGGGAGTCTTGAGGAGACCCCGACTCCAAAGCGGAAACCCCGATGGTGA 300

DB 241 AAGAAATCGGGAGTCTTGAGGAGACCCCGACTCCAAAGCGGAAACCCCGATGGTGA 300

QY 301 GGAGGAGCAATGTGCAATACCAACATGCTGTACTACTGATGGTGTGTAACCACT 360

DB 301 GGAGGAGCAATGTGCAATACCAACATGCTGTACTACTGATGGTGTGTAACCACT 360

QY 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGT 420

DB 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGT 420

QY 421 TATTAAGTCTGTGGTGCAAAAAGACACTTATGCTATGAAAGAGGTTCTTTTATC 480

DB 421 TATTAAGTCTGTGGTGCAAAAAGACACTTATGCTATGAAAGAGGTTCTTTTATC 480

QY 481 TTGGCCAGTATATGACTAAACGATTATATGATGAGAAGCAACAACATTTGATATT 540

DB 481 TTGGCCAGTATATGACTAAACGATTATATGATGAGAAGCAACAACATTTGATATT 540

QY 541 GTTCAATGATCTCTAGGAGATTTGTTGGCGTGCACAGCTTCCTCTGTGGAAGACACA 600

DB 541 GTTCAATGATCTCTAGGAGATTTGTTGGCGTGCACAGCTTCCTCTGTGGAAGACACA 600

QY 601 GGAAATATATACCATGATCTACAGGAACCTTGGTAGTGTAGTCAATCAGCAGGAATCATCG 660

DB 601 GGAAATATATACCATGATCTACAGGAACCTTGGTAGTGTAGTCAATCAGCAGGAATCATCG 660

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DB 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTACCTTGAAGGTGGGAGTGTATCAAAAG 720

QY 1801 AAGAGAAATATATATTTCTTAACATATATATACCCCTAGGAATTTAGACAACCTGAATTTATT 1860
DB 1801 AAGAGAAATATATATTTCTTAACATATATATACCCCTAGGAATTTAGACAACCTGAATTTATT 1860
QY 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTTTAGTATAAT 1920
DB 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTTTAGTATAAT 1920
QY 1921 TGACCTACTTTGGTAGTGAATAGTAATACCTACTATTAATTTGACTTGAATATGTAGCT 1980
DB 1921 TGACCTACTTTGGTAGTGAATAGTAATACCTACTATTAATTTGACTTGAATATGTAGCT 1980
QY 1981 CATCCCTTACACCAACTCTCAATTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
DB 1981 CATCCCTTACACCAACTCTCAATTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
QY 2041 TTGGTTTTTTTTTCTTAATATGATATGACATTTAAATGATAATTTATTTTATT 2100
DB 2041 TTGGTTTTTTTTTCTTAATATGATATGACATTTAAATGATAATTTATTTTATT 2100
QY 2101 AGACCGAGTCTTCTGTTTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
DB 2101 AGACCGAGTCTTCTGTTTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
QY 2161 AGCTCTGCCCTCCCGGGTTCGACCACTTCTCTGCTCAGCCTCCCAATAGCTTGACC 2220
DB 2161 AGCTCTGCCCTCCCGGGTTCGACCACTTCTCTGCTCAGCCTCCCAATAGCTTGACC 2220
QY 2221 TACAGTCACTGCGCACACACCTGGCTGAATTTTGTGACTTTTAGTAGACAGGGTTTC 2280
DB 2221 TACAGTCACTGCGCACACACCTGGCTGAATTTTGTGACTTTTAGTAGACAGGGTTTC 2280
QY 2281 ACCGTGTTAGCCAGGATGCTGATCTCTGACCTCTGATCCGCTGATCCGCGCCCTCC 2340
DB 2281 ACCGTGTTAGCCAGGATGCTGATCTCTGACCTCTGATCCGCTGATCCGCGCCCTCC 2340
QY 2341 CAAAGTCTGGGATACAGCATGACCCACCG 2372
DB 2341 CAAAGTCTGGGATACAGCATGACCCACCG 2372

RESULT 14

US-09-048-810-1
: Sequence 1, Application US/09048810
: Patent No. 6238921
: GENERAL INFORMATION:
: APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
: APPLICANT: Graham, Brett P. Monia
: TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
: TITLE OF INVENTION: MODULATION OF HUMAN MDM2 EXPRESSION
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Law Offices of Jane Massey Licata
: STREET: 66 East Main Street
: CITY: Marlton
: STATE: NJ
: COUNTRY: U.S.A.
: ZIP: 08053
: COMPUTER READABLE FORM:
: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
: COMPUTER: IBM 486
: OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/048,810
: FILING DATE: herewith
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Licata, Jane Massey
: REGISTRATION NUMBER: 32,257
: REFERENCE/DOCKET NUMBER: ISPH-0302
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 609-779-2400

TELEFAX: 609-810-1454
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2372 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Unknown
: ANTI-SENSE: No
: PUBLICATION INFORMATION:
: AUTHORS: Oliner, J.D.
: AUTHORS: Kinzler, K.W.
: AUTHORS: Meltzer, P.S.
: AUTHORS: George, D.L.
: AUTHORS: Vogelstein, B.
: TITLE: Amplification of a gene encoding a
: TITLE: p53-associated protein in human sarcomas
: JOURNAL: Nature
: VOLUME: 358
: ISSUE: 6381
: PAGES: 80-83
: DATE: 02-JUL-1992
: US-09-048-810-1

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCCGGGAGCTTGGCTGCTTCTGGGGCCCTGTGGCCCTGTGTGCGGAAGATGGA 60
DB 1 GCACCCGGGAGCTTGGCTGCTTCTGGGGCCCTGTGGCCCTGTGTGCGGAAGATGGA 60
QY 61 GCAAGAGCGGAGCGCGGAGGGCGGCGGACCCCTCTGACCGAGATCCTGTGCTTTTCG 120
DB 61 GCAAGAGCGGAGCGCGGAGGGCGGCGGACCCCTCTGACCGAGATCCTGTGCTTTTCG 120
QY 121 CAGCGAGGAGCAGCGTCCCTCCCGGATTAGTGGCTACGAGCGCCAGTGCCTGGCCCG 180
DB 121 CAGCGAGGAGCAGCGTCCCTCCCGGATTAGTGGCTACGAGCGCCAGTGCCTGGCCCG 180
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QY 241 AAGGAAGTGGGAGTCTTGAGGAGCCCGGAGTCCAGCGGAAACCCCGGATGGA 300
DB 241 AAGGAAGTGGGAGTCTTGAGGAGCCCGGAGTCCAGCGGAAACCCCGGATGGA 300
QY 301 GGAGCAGGCAAAATGTGCAATACCAATGCTGTACTACTGTGTGTGTAAACACCT 360
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QY 421 TATTAAGTCTGTTGGTGACAAAAGACACTTATATGATGAAAGAGTCTTTTTTATC 480
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DB 601 GGAAATATATATACCATGATCTACAGGAATCTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
QY 661 ACTCAGGTACATCTGTGAGTGAACAGTGTCCACCTTCAAGTGGAGTGTATCAAAAGG 720
DB 661 ACTCAGGTACATCTGTGAGTGAACAGTGTCCACCTTCAAGTGGAGTGTATCAAAAGG 720

Db 661 ACTCAGGTACATCTGTGAGTGTGAGACAGGTGTACCTTGAAGGTGGAGTGATCAAAAGG 720
 Qy 721 ACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780
 Db 721 ACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780
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 Db 841 GTGACGACAAAGAAACCCACAAATCTGATAGTATTTCCCTTTGATGAAGCC 900
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 Db 901 TGCGCTCTGTGTGTAAGGGAGATGTTGTGAAGAGCAGTACGAGTGAATCTACAG 960
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 Db 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATTTGG 1020
 Qy 1021 ATCAGATTCAGTTTCAGATCAGTTTGTAGTGTAGATTTGAAGTGTGAATCTCTCGACTCAG 1080
 Db 1021 ATCAGATTCAGTTTCAGATCAGTTTGTAGTGTAGATTTGAAGTGTGAATCTCTCGACTCAG 1080
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 Db 1081 AAGATTATAGCTTGTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGAGTATATC 1140
 Qy 1141 AAGTTACTGTATCAGGCGAGGAGTGTACAGATTCATTTGAAGAAGTCTCTGAAA 1200
 Db 1141 AAGTTACTGTATCAGGCGAGGAGTGTACAGATTCATTTGAAGAAGTCTCTGAAA 1200
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 Db 1201 TTTCTTGTAGTGTATTTGAAATGACATTCATGCAATGAATCCCTTCCAT 1260
 Qy 1261 CACATTGCAACAGATGTGGGCCCTTCGTGAGAAATTTGGTTCCTGAAAGTAAAGGAAAG 1320
 Db 1261 CACATTGCAACAGATGTGGGCCCTTCGTGAGAAATTTGGTTCCTGAAAGTAAAGGAAAG 1320
 Qy 1321 ATAAAGGGAAATCTCTGAGAAAGCCAACTGAAACTCAACACAGCTGAAGGGCT 1380
 Db 1321 ATAAAGGGAAATCTCTGAGAAAGCCAACTGAAACTCAACACAGCTGAAGGGCT 1380
 Qy 1381 TTGATGTTCTGTATTTGAAAAAATATAGTGAATGATTTCCAGAGAGTATGTTGAGG 1440
 Db 1381 TTGATGTTCTGTATTTGAAAAAATATAGTGAATGATTTCCAGAGAGTATGTTGAGG 1440
 Qy 1441 AAAATGATGATAAAATACACAGCTTCACATCAACAAAGTGAAGACTATTTCTCAGC 1500
 Db 1441 AAAATGATGATAAAATACACAGCTTCACATCAACAAAGTGAAGACTATTTCTCAGC 1500
 Qy 1501 CATCACTTCTAGTAGCATTTATATAGCAGCAAGAGTGAAGAGTTTGAAGGG 1560
 Db 1501 CATCACTTCTAGTAGCATTTATATAGCAGCAAGAGTGAAGAGTTTGAAGGG 1560
 Qy 1561 AAGAAACCCAGCAAGAGAGAGTGTGAATCTAGTTTGGCCCTTAATGTCATTGAAC 1620
 Db 1561 AAGAAACCCAGCAAGAGAGAGTGTGAATCTAGTTTGGCCCTTAATGTCATTGAAC 1620
 Qy 1621 CTTGTGTGATTTGTCAAGGTCGACCTTAAATGTTGCTATTTGCTTCCATGCAAAACAGGAC 1680
 Db 1621 CTTGTGTGATTTGTCAAGGTCGACCTTAAATGTTGCTATTTGCTTCCATGCAAAACAGGAC 1680
 Qy 1681 ATCTTATGGCTTGTATACATGTGCAAGAGCTAAAGAAAGAAATGAAGCCCTGCCAG 1740
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 Qy 1741 TATGTAGCAACCAATTCATGCTGCTAATCTATTTCCCTAGTTGACCTGTCTAT 1800
 Db 1741 TATGTAGCAACCAATTCATGCTGCTAATCTATTTCCCTAGTTGACCTGTCTAT 1800

Qy 1801 AAGAGATATATATTTCTTAACATATATAAACCCTAGGAATTTAGACAACTTGAATTTAT 1860
 Db 1801 AAGAGATATATATTTCTTAACATATATAAACCCTAGGAATTTAGACAACTTGAATTTAT 1860
 Qy 1861 CACATATATCAAAAGTGAGAAATGCGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
 Db 1861 CACATATATCAAAAGTGAGAAATGCGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
 Qy 1921 TGACCTACTTTGGTAGTGGAAATAGTGAATTTACTACTATAATTTGACTTGAATATGAGT 1980
 Db 1921 TGACCTACTTTGGTAGTGGAAATAGTGAATTTACTACTATAATTTGACTTGAATATGAGT 1980
 Qy 1981 CATCTTTTACACCAACCTCAATTTTAAATTTTACTCTCTCTTAAATGAGAAAGTAC 2040
 Db 1981 CATCTTTTACACCAACCTCAATTTTAAATTTTACTCTCTCTTAAATGAGAAAGTAC 2040
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 Db 2041 TTGTTTTTTTTTCTTAAATATATATGATGACATTTAAATGTAATTTATTTTGTG 2100
 Qy 2101 AGACCGAGTCTGTCTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTGTCTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Qy 2161 AGCTCTGCCCTCCCGGGTTGGCACCATTTCTCTGCTCAGCCCTCCCAATTAGCTTGGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTTGGCACCATTTCTCTGCTCAGCCCTCCCAATTAGCTTGGCC 2220
 Qy 2221 TACAGTCACTGCCACCACTGGCTAATTTTGTGCTTTTACTTTTAGTAGACAGAGGTTTC 2280
 Db 2221 TACAGTCACTGCCACCACTGGCTAATTTTGTGCTTTTACTTTTAGTAGACAGAGGTTTC 2280
 Qy 2281 ACCGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTGTATCGGCCACCTCGGCCCTCC 2340
 Db 2281 ACCGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTGTATCGGCCACCTCGGCCCTCC 2340
 Qy 2341 CAAAGTGTGGGATACAGGATGAGCCACCG 2372
 Db 2341 CAAAGTGTGGGATACAGGATGAGCCACCG 2372

RESULT 15
 US-09-170-159A-2
 ; Sequence 2, Application US/09170159A
 ; Patent No. 6399755
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; HILL, DAVID E.
 ; KINZLER, KENNETH W.
 ; VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 13-Oct-1998
 ; CLASSIFICATION: <unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KAGAN, SARAH A.
 ; REGISTRATION NUMBER: 32,141

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Search completed: January 9, 2003, 13:40:56
Job time : 91 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: January 9, 2003, 10:51:14 ; Search time 3329 Seconds
(without alignments)
11539.710 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16134066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 33308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14	519	21.9	555	10 BE296905	BE296905 601176992
15	481.8	20.3	674	10 AW975448	AW975448 EST387557
16	474.2	20.0	578	12 BF435301	BF435301 nab37q05.
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ALIGNMENTS

RESULT 1
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LOCUS Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200011p22;transformed mouse 3T3 cell double minute 2, full insert sequence.
DEFINITION
ACCESSION AK004719
VERSION AK004719.1 GI:12836100
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) adult male lung cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
ORGANISM Mus musculus
clone:1200011p22.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
JOURNAL
MEDLINE
PUBMED 11042159

[illegible]

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DEFINITION	similar to SW:MDM2_HUMAN Q00987 MDM2 PROTEIN ;, mRNA sequence.				
ACCESSION	BF057574				
VERSION	BF057574.1	GI:10811470			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Human sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 709)				
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
COMMENT	Unpublished (1997)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-re@mail.nih.gov				
	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center				
	Clone distribution: NCI-CGAP clone distribution information can be				

found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoimage.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 481.
Location/Qualifiers
source

FEATURES
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BASE COUNT 197 a 163 c 175 g 172 t 2 others
ORIGIN

Query Match 28.6%; Score 679.4; DB 12; Length 709;
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Matches 700; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

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RESULT 6
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ACCESSION BE900427
VERSION BE900427.1 GI:10388579
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SOURCE human.
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 778)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC832 row: h column: 14
High quality sequence stop: 708.
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Location/Qualifiers
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Site:2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Size-selected by
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).".
BASE COUNT 215 a 181 c 203 g 179 t
ORIGIN
Query Match 25.8%; Score 612; DB 12; Length 778;

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Best Local Similarity 92.6%; Pred. No. 3e-106;
Matches 722; Conservative 0; Mismatches 45; Indels 13; Gaps 7;
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Db 712 GCTTCAAGGAAGAAACCTTCTATCTTCAACATTAGGAGCTAAACATATATCTACATCTA 771

RESULT 7
AW500514 612 bp mRNA linear EST 01-MAR-2000
LOCUS UI-HF-BN0-akj-b-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
DEFINITION IMAGE:3077314 5', mRNA sequence.
ACCESSION AW500514
VERSION AW500514.1 GI:7113200
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 612)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

```


Email: cgapbs-re@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/Image/Image.html
 Seq primer: M13 Forward.

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 /cell_type="germinal center B cells"
 /lab_host="DH10B (LTI)"
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 Constructed from size fractionated cytoplasmic mRNA
 (3.5-4.4kb). Directionally cloned. Cells provided by
 Louis M. Staudt, Ph.D. Library preparation by Maria de
 Fatima Bonaldi, Ph.D. and M. Bento Soares, Ph.D."
 BASE COUNT 197 a 103 c 149 g 163 t

Query Match 25.6%; Score 606.4; DB 10; Length 612;
 Best Local Similarity 99.8%; Pred. No. 3.6e-105;
 Matches 607; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 511 ATGATGAGAGCAACACATATTGTATATGTTCAATGATCTCTAGGAGATTGTTG 570
 DB 5 AGGATGAGAGCAACACATATTGTATGTTCAATGATCTCTAGGAGATTGTTG 64
 QY 571 GCGTGCAAGCTTCTCTGTAAGAGCAGCAGGAAATATATACATGATCTACAGAACT 630
 DB 65 GCGTGCAAGCTTCTCTGTAAGAGCAGCAGGAAATATATACATGATCTACAGAACT 124
 QY 631 TGGTAGTAGTCAATCAGCAGGAACTCATCGGACTCAGGTACATCTGTGAGTGAGAACAGGT 690
 DB 125 TGGTAGTAGTCAATCAGCAGGAACTCATCGGACTCAGGTACATCTGTGAGTGAGAACAGGT 184
 QY 691 GTCACCTTGAGCTGGAGTGATCAAGAGGACCTGTACAGAGCTTCAGAGAGAAAC 750
 DB 185 GTCACCTTGAGCTGGAGTGATCAAGAGGACCTGTACAGAGCTTCAGAGAGAAAC 244
 QY 751 CTTCACTTCCACATTTGGTTCTAGACCATCTACCTCATCTAGAGGAGCAATTAGTG 810
 DB 245 CTTCACTTCCACATTTGGTTCTAGACCATCTACCTCATCTAGAGGAGCAATTAGTG 304
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 DB 305 AGACAGAGAAATTCAGATGAATATCTGGTGAACGACAAAGAAACGCCAATACTCG 364
 QY 871 ATAGATTTCCCTTCCCTTTGATGAAGCCTGGCTCTGTGTGTAATAGGAGATATGTT 930
 DB 365 ATAGATTTCCCTTCCCTTTGATGAAGCCTGGCTCTGTGTGTAATAGGAGATATGTT 424
 QY 931 GTGAAGAACAGCTAGCAGTGAATCTACAGGAGCCCATCGAATCCGGATCTTGATGCTG 990
 DB 425 GTGAAGAACAGCTAGCAGTGAATCTACAGGAGCCCATCGAATCCGGATCTTGATGCTG 484
 QY 991 GTGTAGTGAACATTCAGTGATTTGGTGGATCAGGATTCAGTTCAGATCAGTTTAGTG 1050
 DB 485 GTGTAGTGAACATTCAGTGATTTGGTGGATCAGGATTCAGTTCAGATCAGTTTAGTG 544
 QY 1051 TAGAATTTGAAGTTGAATCTCTCGACTCAGAGATTTATAGCCTTAGTCAAGAGGACAAG 1110
 DB 545 TAGAATTTGAAGTTGAATCTCTCGACTCAGAGATTTATAGCCTTAGTCAAGAGGACAAG 604
 QY 1111 AACTCTCA 1118

Db 605 AACTCTCA 612
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 mRNA sequence.
 ACCESSION BI335419
 VERSION BI335419.1 GI:15020076
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 773)
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1346 row: e column: 01
 High quality sequence stop: 771.

FEATURES
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 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 BASE COUNT 212 a 157 c 139 g 265 t

Query Match 25.4%; Score 603; DB 13; Length 773;
 Best Local Similarity 99.0%; Pred. No. 1.5e-104;
 Matches 617; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1200 ATTTCTCTAGCTGACATATGGAATGCATTCATGCAATGAATGAATCCCCCTTCCA 1259
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 QY 1260 TCACATTCACAGAGTTGGGCGCTTCGTGAGATTCGCTTCCTGAAGATAAGGAGAA 1319
 DB 562 TCACATTCACAGAGTTGGGCGCTTCGTGAGATTCGCTTCCTGAAGATAAGGAGAA 503
 QY 1320 GATAAAGGGGAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAAAGCTGAAGAGGC 1379
 DB 502 GATAAAGGGGAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAAAGCTGAAGAGGC 443
 QY 1380 TTTGATCTTCTGATGTAAAAAACTATAGTGAATGATTCAGAGAGTCTATGTTGAG 1439
 DB 442 TTTGATCTTCTGATGTAAAAAACTATAGTGAATGATTCAGAGAGTCTATGTTGAG 383
 QY 1440 GAAATGATGATAAATACAAAGCTTCACAACTCAACAAAGTGAAGACTATTCTCAG 1499
 DB 382 GAAATGATGATAAATACAAAGCTTCACAACTCAACAAAGTGAAGACTATTCTCAG 323
 QY 1500 CCATCACTTCTAGTAGCATTTATTTATAGCAGCCCAAGAGATGTGAAGAGTTTGAAGG 1559
 DB 322 CCATCACTTCTAGTAGCATTTATTTATAGCAGCCCAAGAGATGTGAAGAGTTTGAAGG 263

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Db	262	GAAGAAACCCAAAGACAAAGAGAGTGTGGAAATCTAGTTGCCCTTAATGCCATTGAA	203
Qy	1620	CCTTGTGTCATTTGTCGAAGTTCGACCTAAAAATGGTTGCATTCATCGCAAAACAGGA	1679
Db	202	CCTTGTGTCATTTGTCGAAGTTCGACCTAAAAATGGTTGCATTCATCGCGC-AAACAGGA	144
Qy	1680	CATCTTATGGCGCTGCTTTACATGTGCAGGAAGCTAAAGAAAAGGAATTAAGCCCTGC	1739
Db	143	CATCTTATGGCGCTGCTTTACATGTGCAGGAAGCTAAAGAAAAGGAATTAAGCCCTGC	84
Qy	1740	GTATGTAGACACACCAATTCAAATCATTTGCTACCTATTATTTCCCTAGTTGACCTGTCTA	1799
Db	83	GTATGTAGACACACCAATTCAAATCATTTGCTACCTATTATTTCCCTAGTTGACCTGTCTA	24
Qy	1800	TAAGAGAAATTATATATTCTTAAC	1822
Db	23	TAAGAGAAATTATATATTCTTAAC	1

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DEFINITION	UI-HF-BNO-akj-b-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077318 5', mRNA sequence.
ACCESSION	AW5000516
VERSION	AW5000516.1
KEYWORDS	GI:7113204
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 571)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

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FEATURES
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Location/Qualifiers
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/notes="Vector: pT7r3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic RNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
180 a 96 c 140 g 155 t
BASE COUNT
ORIGIN

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Query Match 23.8%; Score 565.4; DB 10; Length 571;
Best Local Similarity 99.8%; Pred.No. 2.2e-97;
Matches 566; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 511 ATGATCAGAAACCAACAATTTGTATTATTTGTCAAAATGATCTCTPAGAGATTTTTTGG 570
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Db	5	AGSATGAGAGCAACCAATATTTGTTCAAAATGATCTTTCAGGAGATTTGTTTG	64
QY	571	GGGTGCCAAGCTTCTCTGTAAGAGCAGCAAGAAATATATACCATGATCTACAGGAAT	630
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QY	691	GTCACTTGAAGGTGGGAGTGCATCAAAGGACCTTGTACAAGAGCTTTCAGGAGAGAAAC	750
Db	185	GTCACTTGAAGGTGGGAGTGCATCAAAGGACCTTGTACAAGAGCTTTCAGGAGAGAAAC	244
QY	751	CTTCATCTTCACATTTGGTTTCTAGAACCATCTACCTCATCTAGAAGGAGAGCAATTAGTG	810
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QY	811	AGACACAGAAATTCAGATCAATATCTGGTGAACGACAAAGAAACGCCAATCTG	870
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QY	871	ATAGTATTTCCCTTTCCCTTTGATGAAAGCCTGGCTGTGTGTAATAAGGGAGATATGTT	930
Db	365	ATAGTATTTCCCTTTCCCTTTGATGAAAGCCTGGCTGTGTGTAATAAGGGAGATATGTT	424
QY	931	GTGAAGAAGCAGTAGCAGTGAATCTACAGGAGCGCCATCGAATCCGGATCTTGATGCTG	990
Db	425	GTGAAGAAGCAGTAGCAGTGAATCTACAGGAGCGCCATCGAATCCGGATCTTGATGCTG	484
QY	991	GTGTAAGTGAACATTCAGGTCATTTGGTTGGATCAGGATTCAGTTTCAGATCAGTTTAGTG	1050
Db	485	GTGTAAGTGAACATTCAGGTCATTTGGTTGGATCAGGATTCAGTTTCAGATCAGTTTAGTG	544
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RESULT 10
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 ACCESSION
 VERSION
 AWI76629.1
 EST.
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 ORGANISM
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 ILA-CT0079-200899-001-B01 CT0079 Homo sapiens cDNA, mRNA sequence.
 573 bp mRNA linear
 EST 16-NOV-1999

REFERENCE	1 (bases 1 to 573)
AUTHORS	HCGP http://www.ludwig.org.br/ORESTES .
TITLE	The FAPESP/LICR Human Cancer Genome Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Simpson A. J. G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prudente, Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL4&t2=IL4-CT0079-2008&99-001-B01&t3=1999-08-20&st&=1

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High quality sequence stop: 472.
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FEATURES
source
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BASE COUNT 184 a 96 c 137 g 155 t 1 others
ORIGIN

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Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db 61 AAGCTTCTCTGTAAGAGCAGACAGAAATATATACCATGATCTACAGGAATCTGTAGT 120
QY 638 AGTCAATCAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTGAGACAGGTGCACCT 697
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QY 698 TGAAGTGGGAGTATCAAAAGGACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATC 757
Db 181 TGAAGTGGGAGTATCAAAAGGACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATC 240
QY 758 TTCACATTTGGTTTCTAGACCATCTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGA 817
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Db 361 TTCCTTTCTTTGATGAAGCTGGCTCTGTGTGTAATAAGGAGATATTTGTGAAG 420
QY 938 AAGCAGTAGCAGTGAATCTACAGGAGCGCCATCGAATCCGGATCTTGATGCTGGTGAAG 997
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QY 998 TGAACATTCAGGTGATTTGGTGGATCAGGATTCAGTTTCAGATCAGTTTGTAGTAATT 1057
Db 481 TGAACATTCAGGTGATTTGGTGGATCAGGATTCAGTTTCAGATCAGTTTGTAGTAATT 540
QY 1058 TGAAGTTCGAATCTCTGACTCAGAGATTATA 1089
Db 541 TGAAGTTCGAATCTCTGACTCAGAGATTATA 572

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VERSION BE300019.1 GI:9183767
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 964)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
Plate: L1CM53 row: k column: 10
High quality sequence stop: 688.
FEATURES
Location/Qualifiers
1..964
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2960385"
/clone_lib="NIH_MGC_17"
/tissue_type="Rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 309 a 219 c 238 g 198 t
ORIGIN

Query Match 22.6%; Score 535.2; DB 10; Length 964;
Best Local Similarity 90.8%; Pred. No. 1.1e-91;
Matches 739; Conservative 0; Mismatches 53; Indels 22; Gaps 15;
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QY 145 GGATTAGTTCGTACGAGCGCCAGTCGCCCTGGCCGGAGAGTGGAAATGATCCCGGAGGCC 204
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QY 1697 TACATGTGCAAGAGAGTGAAGAAAGGAATAGCCCTGCCAGTATGTAGACAAACCAAT 1756
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DB 302 TCAATGATGTGCTAACTATTATTCCTTGTGCTGCTCTATAGAGAAATATATATT 361

QY 1817 TCTAATATATATACCTPAGAAATTTAGACAACTGAATTTATTCACATATATCAAGTG 1876
DB 362 TCTAATATATATACCTPAGAAATTTAGACAACTGAATTTATTCACATATATCAAGTG 421

QY 1877 AGAAATGCCCTCAATCACAATAGATTTCTCTTTAGTATTAATTTGACCTACTTTGGTAG 1936
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ACCESSION BE296905
VERSION BE296905.1 GI:9180472
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 555)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM207 row: h column: 23
High quality sequence stop: 543.

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/notes="Organ: muscle; Vector: pOB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 133 a 141 c 156 g 125 t
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Query Match 21.9%; Score 519; DB 10; Length 555;
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Matches 550; Conservative 0; Mismatches 5; Indels 8; Gaps 2;

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DEFINITION EST387557 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.
ACCESSION AW975448
VERSION AW975448.1 GI:8166661
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 674)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray

JOURNAL Unpublished (2000)

COMMENT Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208

Email: johnqu@tigr.org

Plate: 349

Seq primer: Forward.

Location/Qualifiers

1..674

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="MAGE resequences, MAGN"

/note="Vector: pbluescriptskm"

BASE COUNT 191 a 165 c 170 g 147 t 1 others

ORIGIN

Query Match 20.3%; Score 481.8; DB 10; Length 674;
Best Local Similarity 81.4%; Pred. No. 1.5e-81;
Matches 658; Conservative 0; Mismatches 8; Indels 142; Gaps 3;

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Qy 262 GGGACCCCGACCTCCAAAGCGCGAAACCCCGGATGGTGGAGCAGGCAAAATGTGCAATA 321
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Job time : 3342 secs

GenCore version 5.1.3
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Run on: January 9, 2003, 11:00:44 ; Search time 107 Seconds
(without alignments)
9756.310 Million cell updates/sec

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Perfect score: 2372
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 389086 seqs, 220051671 residues 778172

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2372	100.0	2372	10	US-09-956-425-7
3	2372	100.0	2372	10	US-09-851-771A-1
4	975.6	41.1	1710	10	US-09-956-425-5
5	652	27.5	652	12	US-10-057-510-3
6	226.4	9.5	148567	10	US-09-801-876B-3
7	226	9.5	1400	10	US-09-263-959-295
8	226	9.5	684973	10	US-09-763-959-1
9	223.2	9.4	22008	10	US-09-764-869-2110
10	223.2	9.4	32185	10	US-09-764-877-3171
11	223	9.4	4978	10	US-09-764-887-355
12	222	9.4	13608	10	US-09-861-846-3
13	222	9.4	41104	10	US-09-816-685-3
14	221.8	9.4	15714	10	US-09-764-869-2355
15	221.8	9.4	32190	10	US-09-764-878-201
16	221.8	9.4	32193	10	US-09-764-878-200
17	221.8	9.4	32249	10	US-09-764-878-202
18	221.4	9.3	32174	9	US-09-860-670-232
19	221.4	9.3	32174	9	US-09-764-904-90

ALIGNMENTS

RESULT 1

US-09-752-983-1

Sequence 1, Application US/09752983

Patent No. US20010016575A1

GENERAL INFORMATION:

APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.

APPLICANT: Graham, Brett P. Monia

TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDN2

TITLE OF INVENTION: EXPRESSION

NUMBER OF INVENTIONS: 271

CORRESPONDENCE ADDRESS:

ADDRESSER: Law Offices of Jane Massey Licata

STREET: 66 East Main Street

CITY: Marlton

STATE: NJ

COUNTRY: U.S.A.

ZIP: 08053

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM PC

OPERATING SYSTEM: WINDOWS 95

SOFTWARE: WORDPERFECT 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/752,983

FILING DATE: 02-Jan-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/280,805

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Licata, Jane Massey

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0346

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-810-1515

TELEFAX: 609-810-1454

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Unknown

Sequence 158, App

Sequence 1134, Ap

Sequence 2645, Ap

Sequence 183, App

Sequence 224, App

Sequence 199, App

Sequence 11, Appl

Sequence 3, Appli

Sequence 1332, Ap

Sequence 1, Appli

Sequence 1, Appli

Sequence 226, App

Sequence 217, App

Sequence 11, Appl

Sequence 1541, Ap

Sequence 1546, Ap

Sequence 1543, Ap

Sequence 1544, Ap

Sequence 7, Appli

Sequence 3, Appli

Sequence 609, App

Sequence 163, App

Sequence 1849, Ap

Sequence 3, Appli

Sequence 3, Appli

ANTI-SENSE: No
 PUBLICATION INFORMATION:
 AUTHORS: Olinier, J.D.
 AUTHORS: Kinzler, K.W.
 AUTHORS: Meltzer, P.S.
 AUTHORS: George, D.L.
 AUTHORS: Vogelstein, B.
 TITLE: Amplification of a gene encoding a
 JOURNAL: Nature
 VOLUME: 358
 ISSUE: 6381
 PAGES: 80-83
 DATE: 02-JUL-1992
 US-09-752-983-1

Query Match 100.0%; Score 2372; DB 10; Length 2372;
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RESULT 2
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 ; Patent No. US20020045192A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kriwacki, Richard
 ; APPLICANT: Bothner, Brian
 ; APPLICANT: Lewis, William
 ; TITLE OF INVENTION: Aif and Hdm2 Interaction Domains and Method of Use Thereof
 ; FILE REFERENCE: 1340/1/035
 ; CURRENT FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 2372
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-956-425-7

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 Db 841 GTGAACGACAAAGAAACGCCACAAATCTGATAGTATTTCCCTTTCCCTTTGATGAAAGCC 900
 QY 901 TGCCCTGTGTGTAATAGGGAGATATTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 Db 901 TGCCCTGTGTGTAATAGGGAGATATTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 QY 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATTTGGTTG 1020
 Db 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATTTGGTTG 1020
 QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGAATTTGAAGTTGAATCTCTCGACTCAG 1080
 Db 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGAATTTGAAGTTGAATCTCTCGACTCAG 1080
 QY 1081 AAGATTATAGCCCTTGTAGTGAAGCAAGAACTCTCAGATGAATGATGAGGTATATC 1140
 Db 1081 AAGATTATAGCCCTTGTAGTGAAGCAAGAACTCTCAGATGAATGATGAGGTATATC 1140
 QY 1141 AAGTTACTGTGTATCAGCGGGGAGTGTATCAGATTCATTTTGAAGAATCCTGAAA 1200
 Db 1141 AAGTTACTGTGTATCAGCGGGGAGTGTATCAGATTCATTTTGAAGAATCCTGAAA 1200
 QY 1201 TTTCCCTTACTGACTGATTTGGAAATGCATTCATGCAATGAAATGAATCCCCCTTCCAT 1260
 Db 1201 TTTCCCTTACTGACTGATTTGGAAATGCATTCATGCAATGAAATGAATCCCCCTTCCAT 1260
 QY 1261 CACATTGCAACAGATTTGGGCCCTTCTGAGAAATTTGGCTTCTGAGATTAAGGGAAG 1320
 Db 1261 CACATTGCAACAGATTTGGGCCCTTCTGAGAAATTTGGCTTCTGAGATTAAGGGAAG 1320

Qy 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAAACTCAACACAGCTGAAGAGGCT 1380
 Db 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAAACTCAACACAGCTGAAGAGGCT 1380
 Qy 1381 TTGATCTTCTCATTTGTAATAAATACTATAGTGAATGATCCAGAGAGTCACTGTGTTGAGG 1440
 Db 1381 TTGATCTTCTCATTTGTAATAAATACTATAGTGAATGATCCAGAGAGTCACTGTGTTGAGG 1440
 Qy 1441 AAAATGATGATAAAATACAAAGCTTCACAAATCAACAAGAAAGTGAAGACTATCTCAGC 1500
 Db 1441 AAAATGATGATAAAATACAAAGCTTCACAAATCAACAAGAAAGTGAAGACTATCTCAGC 1500
 Qy 1501 CATCAACTTCTAGTAGCATTTATATAGCAGCCAAAGAGAGTGAAGAGTTTGAAGGG 1560
 Db 1501 CATCAACTTCTAGTAGCATTTATATAGCAGCCAAAGAGAGTGAAGAGTTTGAAGGG 1560
 Qy 1561 AGAAACCCCAAGCAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
 Db 1561 AGAAACCCCAAGCAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
 Qy 1621 CTTGTGTGATTTGTCAAGTGCAGCTTAAATGGTTGCATTTGCCATTTGCCAAACAGGAC 1680
 Db 1621 CTTGTGTGATTTGTCAAGTGCAGCTTAAATGGTTGCATTTGCCATTTGCCAAACAGGAC 1680
 Qy 1681 ATCTTATGCGCTTCTTACATGTCGAAGAGCTTAAGAAAGAGTAAAGCCCTGCCAG 1740
 Db 1681 ATCTTATGCGCTTCTTACATGTCGAAGAGCTTAAGAAAGAGTAAAGCCCTGCCAG 1740
 Qy 1741 TATGTAGAACCAATCAAAATGATGTGTGTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
 Db 1741 TATGTAGAACCAATCAAAATGATGTGTGTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
 Qy 1801 AAGAGAAATATATATTTCTAATATATAACCTAGGAATTTAGAACACCTGAAATTTAT 1860
 Db 1801 AAGAGAAATATATATTTCTAATATATAACCTAGGAATTTAGAACACCTGAAATTTAT 1860
 Qy 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
 Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
 Qy 1921 TGACCTACTTTGGTAGTGAATAGTGAATTTACTATAATTTGACTTGAATATGAGCT 1980
 Db 1921 TGACCTACTTTGGTAGTGAATAGTGAATTTACTATAATTTGACTTGAATATGAGCT 1980
 Qy 1981 CATCCTTTACACCAACTCTTAATTTAAATATTTCTACTCTCTTAAATGAGAATAC 2040
 Db 1981 CATCCTTTACACCAACTCTTAATTTAAATATTTCTACTCTCTTAAATGAGAATAC 2040
 Qy 2041 TTGGTTTTTTTTTCTTAATATGATATGACATTTAAATGTAATTTATTTTGTG 2100
 Db 2041 TTGGTTTTTTTTTCTTAATATGATATGACATTTAAATGTAATTTATTTTGTG 2100
 Qy 2101 AGACCGAGTCTTCTCTGTTACCCAGGCTGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTTCTCTGTTACCCAGGCTGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Qy 2161 AGCTTCTGCTCCCGGGTTCGACATTTCTGCTGAGCTCCGCTCCCAATGAGCTGGCC 2220
 Db 2161 AGCTTCTGCTCCCGGGTTCGACATTTCTGCTGAGCTCCGCTCCCAATGAGCTGGCC 2220
 Qy 2221 TACAGTCACTGCGACCACTACCTGGCTAAATTTTGTACTTTTGTAGTAGACAGGGTTTC 2280
 Db 2221 TACAGTCACTGCGACCACTACCTGGCTAAATTTTGTACTTTTGTAGTAGACAGGGTTTC 2280
 Qy 2281 ACCGTGTAGCCAGGATGCTCTGATCTCCGACCTCGATCGCTGATCGGCTCC 2340
 Db 2281 ACCGTGTAGCCAGGATGCTCTGATCTCCGACCTCGATCGCTGATCGGCTCC 2340
 Qy 2341 CAAAGTCTGGGATTAACAGGCAATGAGCCACCG 2372
 Db 2341 CAAAGTCTGGGATTAACAGGCAATGAGCCACCG 2372

RESULT 3
 US-09-851-771A-1
 : Sequence 1, Application US/09851771A
 : Patent No. US20020151511A1
 : GENERAL INFORMATION:
 : APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
 : : Graham, Brett P. Monla
 : TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
 : : MODULATION OF HUMAN MDM2 EXPRESSION
 : NUMBER OF SEQUENCES: 32
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Law Offices of Jane Massey Licata
 : STREET: 66 East Main Street
 : CITY: Marlton
 : STATE: NJ
 : COUNTRY: U.S.A.
 : ZIP: 08053
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 : COMPUTER: IBM 486
 : OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
 : SOFTWARE: WORDPERFECT 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/851,771A
 : FILING DATE: 09-May-2001
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 09/048,810
 : FILING DATE: 1998-03-26
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Licata, Jane Massey
 : REGISTRATION NUMBER: 32,257
 : REFERENCE/DOCKET NUMBER: ISPH-0302
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 609-779-2400
 : TELEFAX: 609-810-1454
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2372 base pairs
 : TYPE: Nucleic Acid
 : STRANDEDNESS: Single
 : TOPOLOGY: Unknown
 : ANTI-SENSE: NO
 : PUBLICATION INFORMATION:
 : AUTHORS: Oliner, J.D., Kinzler, K.W., Meltzer, P.S., George, D.L., Vogelstein, B.
 : TITLE: Amplification of a gene encoding a p53-associated protein in
 : JOURNAL: Nature
 : VOLUME: 358
 : ISSUE: 6381
 : PAGES: 80-83
 : DATE: 02-JUL-1992
 : SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 : US-09-851-771A-1
 :
 : Query Match 100.0%; Score 2372; DB 10; Length 2372;
 : Best Local Similarity 100.0%; Pred. No. 0;
 : Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 : QY 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCCTGTGGCCCTGTGTCGCGAAAGATGA 60
 : DB 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCCTGTGGCCCTGTGTCGCGAAAGATGA 60
 : QY 61 GCAAGAAAGCGAGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 : DB 61 GCAAGAAAGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 : QY 121 CAGCAGCAGCAGCGCTCCCTCCCGGATGAGTGCCTAGCAGCGCCAGTCCCTGCCGCG 180
 : DB 121 CAGCAGCAGCAGCGCTCCCTCCCGGATGAGTGCCTAGCAGCGCCAGTCCCTGCCGCG 180
 : QY 181 GAGAGTGAATGATCCCGAGGCCCGCAGGCGCTGCTGCTCCGCGAGTAGTCAGTCCCGCG 240
 : DB 181 GAGAGTGAATGATCCCGAGGCCCGCAGGCGCTGCTGCTCCGCGAGTAGTCAGTCCCGCG 240

Db 181 GAGGTGGGAATGATCCCGAGGCCAGGGCGTGTGCTTCCGCACTAGTCACTAGTCCCGGTG 240
Qy 241 AAGGAACTGGGGAGTCTTGGAGGACCCCGACTCAAGCGGGAAGAACCCCGGATGTGA 300
Db 241 AAGGAACTGGGGAGTCTTGGAGGACCCCGACTCAAGCGGGAAGAACCCCGGATGTGA 300
Qy 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACTACTGATGGTCTGTAAACCACT 360
Db 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACTACTGATGGTCTGTAAACCACT 360
Qy 361 CACAGATCCAGCTTCGGAACAGAGACCTGGTTAGACCAAGCAATGCTTTTGAAGT 420
Db 361 CACAGATCCAGCTTCGGAACAGAGACCTGGTTAGACCAAGCAATGCTTTTGAAGT 420
Qy 421 TATTAAGTCTGTGGTCACAAAAGACACTTATACTATGAAGAGTCTTTTTTATC 480
Db 421 TATTAAGTCTGTGGTCACAAAAGACACTTATACTATGAAGAGTCTTTTTTATC 480
Qy 481 TTGGCCAGPATATATGACTAAAGCAATPATATGATGAGAGCAACACATATTTATTT 540
Db 481 TTGGCCAGPATATATGACTAAAGCAATPATATGATGAGAGCAACACATATTTATTT 540
Qy 541 GTTCAAAATGATCTTCTAGGAGATTTGTTGGCGTGCCAAAGCTTCTCTGTGAAGAGCACA 600
Db 541 GTTCAAAATGATCTTCTAGGAGATTTGTTGGCGTGCCAAAGCTTCTCTGTGAAGAGCACA 600
Qy 601 GGAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
Db 601 GGAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
Qy 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTCACTTTCACATTTGGTTCTTAGAGCAT 780
Db 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTCACTTTCACATTTGGTTCTTAGAGCAT 780
Qy 721 ACCTTGTACAGAGCTTCAGAACAGAAACCTTTCATCTTCACTTTGCTTCTAGACCAT 780
Db 721 ACCTTGTACAGAGCTTCAGAACAGAAACCTTTCATCTTCACTTTGCTTCTAGACCAT 780
Qy 781 CTACCTCATCTAGAGGAGCAATTAGTGAGACAGAACAAATTCAGATGAATATCTG 840
Db 781 CTACCTCATCTAGAGGAGCAATTAGTGAGACAGAACAAATTCAGATGAATATCTG 840
Qy 841 GTGAACGACAAAGAACGCCCAAAATCTGATAGTATTTCCCTTTCCCTTTGATGAAGCC 900
Db 841 GTGAACGACAAAGAACGCCCAAAATCTGATAGTATTTCCCTTTCCCTTTGATGAAGCC 900
Qy 901 TGGCTCTGTGTAAATAGGGAGATATGTTGTGAAGAGAGCAGTAGCAGTGAATCTACAG 960
Db 901 TGGCTCTGTGTAAATAGGGAGATATGTTGTGAAGAGAGCAGTAGCAGTGAATCTACAG 960
Qy 961 GGAGCCATCGAATCCGATCTTCACTGCTGATGATGATGATGATGATGATGATGATGATG 1020
Db 961 GGAGCCATCGAATCCGATCTTCACTGCTGATGATGATGATGATGATGATGATGATGATG 1020
Qy 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAGAATTTGAAGTTTGAATCTCTGACATCAG 1080
Db 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAGAATTTGAAGTTTGAATCTCTGACATCAG 1080
Qy 1081 AAGATTATAGCTTGTAGTAGAAGGACAAAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
Db 1081 AAGATTATAGCTTGTAGTAGAAGGACAAAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
Qy 1141 AAGTTACTGTATCAGCAGGAGAGTATACAGATTCATTTGAAGATCCTGAAA 1200
Db 1141 AAGTTACTGTATCAGCAGGAGAGTATACAGATTCATTTGAAGATCCTGAAA 1200
Qy 1201 TTTCCCTTAGCTATTTGGAAATGCACTTCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1260
Db 1201 TTTCCCTTAGCTATTTGGAAATGCACTTCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1260
Qy 1261 CACATTCGAACAGATGTTGGGCGCTTCTGAGAAATGGGCTTCTGAAATGAAGAGGAAAG 1320
Db 1261 CACATTCGAACAGATGTTGGGCGCTTCTGAGAAATGGGCTTCTGAAATGAAGAGGAAAG 1320

Qy 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACACAACTGGAAGAGGGCT 1380
Db 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACACAACTGGAAGAGGGCT 1380
Qy 1381 TTGATGTTCCCTGATTTGAAAAAATATAGTGAATGATTCAGAGAGTCAATGTTGAGG 1440
Db 1381 TTGATGTTCCCTGATTTGAAAAAATATAGTGAATGATTCAGAGAGTCAATGTTGAGG 1440
Qy 1441 AAAATGATGATAAATAACAAAGCTTCAATCAAGAAAGTGAAGACTATTCACAG 1500
Db 1441 AAAATGATGATAAATAACAAAGCTTCAATCAAGAAAGTGAAGACTATTCACAG 1500
Qy 1501 CATCAACTCTAGTAGCATTTATTTAGCAGCAAGAGATGTGAAGAGTTGAAGGG 1560
Db 1501 CATCAACTCTAGTAGCATTTATTTAGCAGCAAGAGATGTGAAGAGTTGAAGGG 1560
Qy 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
Db 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
Qy 1621 CTTGTGTGATTTGTCAGAGTCTGACCTTAAATAATGTTGCAATGTCATGTCATGTCAT 1680
Db 1621 CTTGTGTGATTTGTCAGAGTCTGACCTTAAATAATGTTGCAATGTCATGTCATGTCAT 1680
Qy 1681 ATCTTATGGCCTGCTTTACATGTGCAAGAGCTTAAAGAAAGATTAAGCCCTGCCAG 1740
Db 1681 ATCTTATGGCCTGCTTTACATGTGCAAGAGCTTAAAGAAAGATTAAGCCCTGCCAG 1740
Qy 1741 TATGTAGAACCAATTCAAATGATTTGCTAACTTATTTCCCTTAGTGTGACCTGTCTAT 1800
Db 1741 TATGTAGAACCAATTCAAATGATTTGCTAACTTATTTCCCTTAGTGTGACCTGTCTAT 1800
Qy 1801 AAGAGAAATATATTTCTAACTATATAACCTTAGGAATTTAGACAACCTGAATTTATT 1860
Db 1801 AAGAGAAATATATTTCTAACTATATAACCTTAGGAATTTAGACAACCTGAATTTATT 1860
Qy 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
Db 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
Qy 1921 TGACCTACTTTGGTAGTGGAAATAGTGAATCTACTATAATTTGACTTTGAATATGACT 1980
Db 1921 TGACCTACTTTGGTAGTGGAAATAGTGAATCTACTATAATTTGACTTTGAATATGACT 1980
Qy 1981 CATCTCTTACACCAACTCCTAAATTTAAATAATTTCTACTCTGCTTAAATGAGAAGTAC 2040
Db 1981 CATCTCTTACACCAACTCCTAAATTTAAATAATTTCTACTCTGCTTAAATGAGAAGTAC 2040
Qy 2041 TTGGTTTCTTTTCTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
Db 2041 TTGGTTTCTTTTCTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
Qy 2101 AGACCGAGCTTGGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2101 AGACCGAGCTTGGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Qy 2161 AGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Db 2161 AGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Qy 2221 TACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Db 2221 TACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Qy 2281 ACCGTGTTAGCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Db 2281 ACCGTGTTAGCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Qy 2341 CAAAGTCTGGGATTAACAGGATGAGCCAGC 2372
Db 2341 CAAAGTCTGGGATTAACAGGATGAGCCAGC 2372

REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 295:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-295

Query Match 9.5%; Score 226; DB 10; Length 1400;
Best Local Similarity 85.2%; Pred. No. 5e-41;
Matches 276; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

QY 2050 TTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTATTTTGTGAGACCGAGT 2109

DB 380 TTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTGAGACCGAGT 439

QY 2110 CTGCTCTGTACCCAGCGTGGAGTGCAGTGG-GTGATCTTGGCTCACTGCAAGCTCTGC 2168

DB 440 CTCGCTCTGTCCCGAGCGTGGAGTGCAGTGGCGGCTCACTGCAAGCTCTGC 499

QY 2169 CTTCCCGGGTTCGCGACATTCCTGCTCAGCTCCCAATTAAGCTTGGCTACAGTCA 2228

DB 500 C--TCCCGGGTTCAGCGCATTCCTGCTCAGCTCCCGAGTACGCGGAGTACAGGCG 557

QY 2229 TCTGCCACACACCTTGCTCAATTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGT 2288

DB 558 CCGCGCACACCGCGCTCAATTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGT 617

QY 2289 AGCAGGATGTCGATCTCTGATCTGATCGCGCCACCTCGGCTCCCAAGTGC 2348

DB 618 ACCAGGATGTCGATCTCTGATCTGATCGCGCCACCTCGGCTCCCAAGTGC 677

QY 2349 TGGGATTACAGCGATGAGCCACCG 2372

DB 678 TGGGATTACAGCGATGAGCCACCG 701

RESULT 8

US-09-263-959-1

Sequence 1, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Rowen, Lee

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:

ADDRESS: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

FILING DATE: 05-MAR-1999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 920010.426C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684973 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-1

Query Match 9.5%; Score 226; DB 10; Length 684973;
Best Local Similarity 85.2%; Pred. No. 5.5e-40;
Matches 276; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

QY 2050 TTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTGAGACCGAGT 2109

DB 172880 TTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTGAGACCGAGT 172939

QY 2110 CTGCTCTGTACCCAGCGTGGAGTGCAGTGG-GTGATCTTGGCTCACTGCAAGCTCTGC 2168

DB 172940 CTCGCTCTGTCCCGAGCGTGGAGTGCAGTGGCGGCTCACTGCGGCTCACTGCAAGCTCTGC 172999

QY 2169 CTTCCCGGGTTCGCGACATTCCTGCTCAGCTCCCAATTAAGCTTGGCTACAGTCA 2228

DB 173000 C--TCCCGGGTTCAGCGCATTCCTGCTCAGCTCCCGAGTACGCGGAGTACAGGCG 173057

QY 2229 TCTGCCACACACCTTGCTCAATTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGT 2288

DB 173058 CCGCGCACACCGCGCTCAATTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGT 173117

QY 2289 AGCAGGATGTCGATCTCTGATCTGATCGCGCCACCTCGGCTCCCAAGTGC 2348

DB 173118 AGCAGGATGTCGATCTCTGATCTGATCGCGCCACCTCGGCTCCCAAGTGC 173177

QY 2349 TGGGATTACAGCGATGAGCCACCG 2372

DB 173178 TGGGATTACAGCGATGAGCCACCG 173201

RESULT 9

US-09-764-869-2110

Sequence 2110, Application US/09764869

Patent No. US20020061521A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC007

CURRENT APPLICATION NUMBER: US/09/764,869

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 2442

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 2110

LENGTH: 22008

TYPE: DNA

ORGANISM: Homo sapiens

US-09-764-869-2110

Query Match 9.4%; Score 223.2; DB 10; Length 22008;

Best Local Similarity 85.5%; Pred. No. 6.1e-40;

Matches 272; Conservative 0; Mismatches 43; Indels 3; Gaps 2;

QY 2056 TTAATATGATATGACATTTAAATGTAATTTATTTTGTGAGACCGAGTCTTGT 2115

DB 3451 TTAGGTAGATAGATGAGTGTGATAGATTTATTTTGTGAGACCGAGTCTTGT 3510

QY 2116 CTGTTACCCAGCGTGGAGTGCAGTGG-GTGATCTTGGCTCACTGCAAGCTCTGCCCTCCC 2174

DB 3511 CTGTTGCCAGCGTGGAGTGCAGTGGGACGATCTCGGCCACTGCAAGCTCTCACCTT-C 3568

QY 2175 CGGGTTCGACCATTCCTGCTCAGCTCCCAATTAAGCTTGGCTTACATCTGCC 2234

DB 3569 CAGGTTACACACCTCTCTGCTCAGCTCCCGAGTACGCTGGGACACAGCGCTACC 3628

QY 2235 ACCACACCTGGCTAATTTTGTACTTTAGTAGACAGAGGCTTACCGGTGTAGCCAG 2294
DB 3629 ACCACGCTGGCTAATTTTGTATTTTATTTAGTAGACAGGGGTTTACCGGTGTAGCCAG 3688
QY 2295 GATGGTCTCGATCTCTGACCTGTGATCGGCCACCTCGGCTCCCAAGTGTGGGAT 2354
DB 3689 GATGGTCTCGACCTCTGACCTGTGATCGGCCACCTCGGCTCCCAAGTGTGGGAT 3748
QY 2355 TACAGGATGAGCCACC 2372
DB 3749 TACAGGATGAGCCACC 3766

RESULT 10

US-09-764-877-3171
; Sequence 3171, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3171
; LENGTH: 32185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3171

Query Match 9.4%; Score 223.2; DB 10; Length 32185;
Best Local Similarity 83.4%; Pred. No. 7e-40;
Matches 277; Conservative 0; Mismatches 53; Indels 2; Gaps 2;

QY 2041 TTGGTCTTTTCTTAATATCTATATGACATTTAAATGTAACCTATATTTTGTG 2100
DB 4482 TTTCATCTGTTTATATATATTTACTTTTAAAGTAGCTTTTATTTTITG 4541
QY 2101 AGACAGGATCTGCTCTTTACCCAGCTGGAGTGCAGTGG-GTATCTTGGCTCACTGC 2159
DB 4542 AGACAGGATCTGCTCTCTGCCAGCTGGAGTGCAGTGGAGTCTCGGCTCACTGC 4601
QY 2160 AAGCTCTGCCCTCCCGGGTTTCGACCATTTCTCTGCTCCATGCCCTCCCAATAGCTTGGC 2219
DB 4602 AGGCTCCGCC-CCCGGGTTTACGCCATTTCTCTGCTCCATGCCCTCCCAATAGCTTGGG 4660
QY 2220 CTACAGTATCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGACAGAGGTTT 2279
DB 4661 CTACAGGCTCCGCCACCTCCCGGCTAATTTTGTATTTTGTAGAGATGGGTTT 4720
QY 2280 CACCGTGTAGCAGAGTGTCTGATCTCTGACCTGTGATCGGCCACCTCGGCTC 2339
DB 4721 CACCGTGTAGCAGAGTGTCTGATCTCTGACCTGTGATCGGCCACCTCGGCTC 4780
QY 2340 CCAAGTGTGGGATTACAGGATGAGCCACC 2371
DB 4781 CCAAGTGTGGGATTACAGGATGAGCCACC 4812

RESULT 11

US-09-764-887-355/C
; Sequence 355, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA113
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 355
; LENGTH: 4978
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-355

Query Match 9.4%; Score 223; DB 10; Length 4978;
Best Local Similarity 85.0%; Pred. No. 3.8e-40;
Matches 273; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

QY 2052 TTTCTTAAATATGTATATGACATTTAAATGTAACCTATATTTTGTAGACAGGCTCT 2111
DB 2861 TGTCCACCAA 2802
QY 2112 TGCTCTGTATCCAGGCTGGAGTGCAGTGG-GTGATCTTGGCTCACTGCAAGCTCTGCC 2170
DB 2801 CGCTCTGTATCCAGGCTGGAGTGCAGTGGCGGATCTTGGCTCACTGCAAGCTC--CAC 2744
QY 2171 TCCCGGGTTCGCACCATTTCTCTGCTCAGCTCCCAATTAGCTTGGCTTACAGTCACTC 2230
DB 2743 CTCCCGGGTTCAGGCCATTTCTCTGCTCAGCTCCCGAGTAGCTGGAGCTACAGCGGCC 2684
QY 2231 TGCCACCACTGCTGCTAATTTTGTACTTTTGTAGACAGAGGTTTACCGGTGTAG 2290
DB 2683 CGCCACCACTGCTGCTAATTTTGTACTTTTGTAGACAGAGGTTTACCGGTGTAG 2624
QY 2291 CCAGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTCGGCTTCCCAAGTCTG 2350
DB 2623 CCAGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTCGGCTTCCCAAGTCTG 2564
QY 2351 GGATTACAGGATGAGCCACC 2371
DB 2563 GGATTACAGGATGAGCCACC 2543

RESULT 12

US-09-861-846-3
; Sequence 3, Application US/09861846
; Patent No. US20020110852A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001065
; CURRENT APPLICATION NUMBER: US/09/861,846
; PRIOR FILING DATE: 2001-05-22
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 13608
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(13608)
; OTHER INFORMATION: n = A,T,C or G
US-09-861-846-3

Query Match 9.4%; Score 222; DB 10; Length 13608;
Best Local Similarity 90.3%; Pred. No. 9.3e-40;
Matches 260; Conservative 0; Mismatches 25; Indels 3; Gaps 2;

QY 2086 TTATTATTTTGTAGACAGGATCTTGTCTCTATTACCCAGGCTGGAGTGCAGTGG-GTG 2144
DB 6767 TTTTATTTTGTAGACAGGATCTTGTCTCTATTACCCAGGCTGGAGTGCAGTGGGCT 6826
QY 2145 ATCTTGGCTCACTGCAAGCTCTGCCCTCCCGGGTTTCGACCATTTCTCTCCCTCAGCT 2204
DB 6827 ATCTTGGCTCACTGCAAGCTCTGCC--TCCAGGTTTCAGCCATTTCTCTCCCTCAGCT 6884

[illegible]



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